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31.7%; Score 32;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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APPLICATION NUMBER: 60/0
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REGISTRATION NUMBER:
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INFORMATION FOR SEQ ID NO:
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COUNTRY: USA
ZIP: 19103-2793
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SIREET: 40
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/cgn2_6/ptodata/1/ina/PCIUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCIUS_COMB.seq:*
                GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Sequence 103, Appli
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4000 Bell Atlantic Tower, 1717 Arch Stre
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US-08-633-879C-17
US-08-368-281-1
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US-08-02-056-6
US-08-07-02-056-5
US-08-07-02-05-5
US-08-08-05-58-5
US-08-802-627A-5
US-08-801-238-5
US-08-801-238-5
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US-09-104-296-5
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APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Lewis, Ceri J.
IIILE OF INVENTION: No. 6150340el Compounds
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFIWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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FILING DATE:
CLASSIFICATION:
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FILING DATE: 28-APR-1997
ATIORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 60/037,857
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: 60/044,365
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DB 3; Length 300;

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CLASSIFICATION:
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US-08-951-527-175/c
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                           RESULT 3
US-09-010-232-1/C
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US-09-010-232-1
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68.8%; Pred. No. 0.19;
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4000 Bell Atlantic Tower, 1717 Arch Stre
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APPLICANT: Black, Michael T.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Lawlor, Elizabeth J.
TILLE OF INVENTION: No. 6200774el Compounds
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DAIR:
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FP: GM50027
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APPLICATION NUMBER: 60/044,365
FILING DATE: 28-APR-1997
APPLICATION NUMBER: 60/044,366
FILING DATE: 28-APR-1997
ATTORNEY,AGENT INPORMATION:
NAME: FAIK, SLEPHEN I
REGISTRATION NUMBER: 36,795
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APPLICATION NUMBER: 60/037,857
FILING DATE: 07-FEB-1997
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 300 base pairs
IYPE: nucleic acid
STRANDEDNESS: double
Best Local Similarity 68.8 Matches 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19103-2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                             98 AGIT 101
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US-09-010-233-5/C
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GENERAL INFORMATION:
APPLICANT: Charles Kunsch
IIILE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                   E: Dechert, Price & Rhoads
4000 Bell Atlantic Tower, 1717 Arch Stre
                                                GENERAL INFORMATION:
APPLICANT: Black, Michael I.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Lewis, Ceri J.
IIILE OF INVENTION: No. 6248557el Compounds
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 31.7%; Score 32; DB 4;
Best Local Similarity 68.8%; Pred. No. 0.19;
Matches 44; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERAIING SYSTEM: DOS
SOFIWARE: FastEBO for Windows Version 2.0
CURRENT APPLICATION DAIA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/010,232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/937,857
APPLICATION NUMBER: 60/937,857
APPLICATION NUMBER: 60/044,366
FILING DATE: 28-APR-1997
APPLICATION NUMBER: 60/044,365
FILING DATE: 28-APR-1997
ATTORNEY/AGENT INFORMATION:
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Patent No. 6420135
Sequence 1, Application US/09010232
Patent No. 6248557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
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LENGTH: 300 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM IYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Falk, Stephen T
REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX 215-994-2222
                                                                                                                                                                                            CORRESPONDENCE ADDRESS: ADDRESSEE: Dechert,
                                                                                                                                                                                                                                                                   Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CON OPERALING SYSTEM: SOFTWARE: FASTSE
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32 51.7 570 13 B1820394 32 51.7 668 17 BH788691 .6 31.3 403 17 FR0023141 .6 31.3 435 9 AL72759 .6 31.3 555 17 AQ681385 .6 31.3 578 9 AL514767 .6 31.3 911 17 A0889744	31.4 31.1 554 17 AQ931126 31.2 30.9 514 17 AR986030 31.2 30.9 514 17 AZ638018 31.2 30.9 535 17 AZ638018	31.2 30.9 692 17 BH834121 31.2 30.9 728 17 BH826507 31.2 30.9 808 13 BIO88828	2 30.9 900 9 ALS4/213 1 30.7 1123 12 85701181 1 30.7 414 17 A2868761 1 30.7 645 17 20.556131	26 31 30.7 881 17 M2530131 27 31 50.7 911 17 AZ532286 28 31 30.7 1101 17 CNS01501 28 30 30.7 1101 17 CNS01501	30.8 30.5 349 10 ANI/2083 30.8 30.5 312 17 A0765687	30.8 30.5 721 12 BG762662 30.8 36.5 855 17 CNS012BX 30.6 30.3 106 12 BER27565	30.0 50.3 462 9 ALSIATAS 30.6 30.3 534 17 AQ735325 30.6 30.3 593 17 AQ531230 30.6 30.3 596 17 RH265245	30.6 30.3 713 17 A2623576 30.6 30.3 760 17 A2628465 30.6 30.3 1067 17 AG029559	10 AW177337 10 AW177341 10 AW177381 10 AW177379	TS	RESULT 1. AA421341/C AA421341 LCJUS AA421341 DEFINITION ZUGGBLIT SOMTES LESTIS, NHT HOMO SAPIENS CDNA CLONE IMAGE:731651 S similar to 99.X51602_cds VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTER 1 (HIMAN).	GI:2100333		AUTHORS Hiller, L., Allen, M., Bowles, L., Dubuque Krizman, D., Kucaba, T., Lacy, M., Le, N., I., J., Moore, B., Schellenberg, K., Steptoe,	tterston,R. and Wilson,R. roject	Mashington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 1e1: 314 286 1800 Fax: 314 286 1810 Email: setwarson.wustl.edu This close is available royalty-free through LENL; contact the IMAGE Consortium (incolmage.lini.gov) for further information. Insert Length: 801 Std Error: 0.00
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd. Nucleic - nucleic search, using SW model	December 8, 2002, 05:54:0	<pre>1111e: US-U9-7/8-900A-5_COPY_500_600 Perfect score: 101 Sequence: 1 atatggtgcctgtggtctcctatgtaaatgcttccaagtt 101</pre>	Scoring table: IDENTITY_NUC Gapext 1.0 Gapop 10.0 , Gapext 1.0 Searched: 16154066 segs, 8097743376 residues	isfying	Maximum DB seq length: 200000000	rost-processing: Minimum Match U% Maximum Match 100% Listing first 45 summaries	Database : EST:* 1: em_estba:* 2: em_esthum:*	910.9.	0: em_estpl:* 7: em_estro:* 8: em_htc:* 9: 9b = estl:*				26: em_gss_pro:	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Result Query No. Score March DR 1D	101 100.0 432 9 74.4 5 513 17 33.2 32.9 232 17 33.2 32.9 508 17 33 32.7 476 17 32.2 31.9 1197 12

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/db_xref="taxon:3702"
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                       /lab_host="DH103"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH757424.1 GI:19041281
                                                                                                                                                                                                                                                           73.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thallana
                                                                                                                                                                                                                                                                                           86; Conservative
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ORIGIN
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                                                                                                                                                                               A1025332 A1025332 A1025332 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643052 similar to 9b:X51602_cds1 VASCULAR ENDOIHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email cgapbs-rémail.nin.gov CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaido
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Netazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 513)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/IINL ac:
www.bio.lnl.gov/bbry/image/image.html
Insert Length: 841 Std Error: 0.00
Seg primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 TCTTTCTGTTTCTTCATTAGATATGTAAATGCTTTCAAGTT 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                         Score 101; DB 9;
Pred. No. 6.4e-15;
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 346.
Location/Qualifiers
                                                                                                               /clone="lMAGE:731061"
/clone_lib="Soares_testis_NHT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                 /organism="Homo sapiens"
/db_xref="GDB:5927885"
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/db_xref="taxon:9606"
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                                                                                                   /db_xref="taxon:9606"
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                                                                                                                                                                    /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 101; Conservative
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TITLE
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AI025332
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KEYWORDS
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                                   FEATURES
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/note="Vector: pI7I3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
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A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html*
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more IDNA insertion
elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is single pass sequence recovered from the left border of IDNA. This sequence lies within 300 bases of the 3' end of At5g05150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 ATAIGGGGCCIGIGGICCTGCTGACTAGAGCTGGCTTTICCTGTCTGATAAT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH757424 13.00.x Arabidopsis thaliana IDNA insertion lines Arabidopsis thaliana genomic clone SALK_056184.53.00.x, DNA Arabidopsis thaliana genomic clone SALK_056184.53.00.x, DNA
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis;
1 (bases 1 to 232)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 513;
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 74.4; DB 9;
Pred. No. 1.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Alab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
Alab_host="Vector: PWD42nv; Purified genomic DNA from M.
Musculus GS7BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch or liftee at constant velocity. The sheared bNA
was blunt end-repaired with T4 DNA polymerase and T4
polymusleotide kinase. Adaptor oligonaleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 &b range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil47321141gb[AR129072.1), a copy number
inducible derivative of plasmid R1. Inc vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse LNA was annealed to
adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                  A2805047 476 bp DNA linear GSS 20-FEB-2001
2M0072E19R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.  
                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 476)
                                                                                                                                                                                                                                                                                                                   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duvai, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Federsen, T., Reilly, M., Rose, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Emāil: ddunnēgenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0072 row; E column: 19
                                                                                                                  clone UUGC2M0072E19 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seg primer: CACACAGAAACAGGTATGACC
Class: plasmid ends
High quality sequence stop: 476.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="dugc2M0072E19"
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                                                                                                                                                           A2809047.1 GI:12975012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                             house mouse.
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                       RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Primates; Catarrhini; Hominidee; Homo. 1 (bases 1 to 508) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., 2hao, S., Adams, M.D. and Hood, L.
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Clones may be purchased from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dclone="Plate=3001 Col=3 Row=C"
/clone_lim="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: sperm; Vector: pBeloBACil; BAC Clones in E-Coli DH10B"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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                                                                Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3887
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Plate: 3001 row: C column: 3
  15 others
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                                                                Score 33.2; DB 17;
Pred. No. 1.7e+02;
                                                                                                             0; Mismatches 33;
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University of Washington
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Location/Qualifiers
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40 g
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                                                                  32.98;
61.68;
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  25
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Class: BAC ends
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AQ779483/c
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/note="Organ: pooled brain, lung, testis; Vector:
pcWw-SPORT6; Site_1: NotI: Site_2: EccRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27: and 1 male testis, age 69. Library is
oligo-dT primed and directionally closed (EccRV site*);
destroyed upon cloning). Average insert site 1:8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
duber (Invitrogen). Research Genetics tracking code
(21. Note: this a NHH_MGC Library."
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Bukaryota, Marazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchoceroidae: Brugia.

1 (bases 1 to 668)
Whitcon, C., Paub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Foster
J., Guillano,D., Slatko,B. and Blaxter,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BH768651 6S8 20-MAR-2002 BMBAC361D117_PSU Brugia malayi Genomic Bac Library 3 Brugia malayi
                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The T.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                               1 (bases 1 to 570)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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http://image.llnl.gov
Plate: LLAM1141 row: h column: 21
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Institute of Cell, Animal and Population Biology
University of Edinburgh
                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:5177156"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 451.
Location/Qualifiers
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BH768691.1 GI:19566455
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                                Homo sapiens
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                                                                                                                                                                                   EST 03-APR-2001
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B1820394
E8820394.1 GI:15931944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov/
Plate: LLCMI502 row: k column: 16
High quality sequence stop: 237.

Location/Qualifiers

1. 1197
                                                                                                                                                                             BG588053 1197 bp mRNA linear EST 03-APR-602863562Fl NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4688391 5'
                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1197)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 TIAGAGCTGGATGCCTTTTCCTGTTAATTCTTTCTGTTTCTTCTTAGATATGTA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-rémail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboracories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_77"
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77 TIAGATATGTAAATGCTTTCA 97
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Best Local Similarity
Matches 46, Conserve
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/clone="089H11ac2"
/clone_lib="cosmid 089H11"
/ 76 c 81 9 102 t
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/clone="BNOAA088ZF04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F.rubripes GSS sequence, clone 089H11aC2, genomic survey sequence. ALO16000.1 GI:2682368
                                 Tel: +44 131 650 6760

Fax: +44 131 670 5450

Fax: +44 131 670 5450

Famil: mark.blaxter/ed.ac.uk

Sequenced from the Brugia malayi BAC library constructed by Claire
Whitton and Dr Mike Quail. The sequence was generated by The
Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
Seq primer: T7 (TAATACGACTCACTATAGGG)

Class: BAC ends.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Ashworth Labs, King's Buildings, West Mains Road, Edinburgn, EHS
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/clone_lib="Brugia malayi Genomic Bac Library 3"
/sex="Mixed (male and female)"
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Live 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                             /tissue_type="whole parasite"
/dev_stage="microfilaria (L1)"
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/db_xref="taxon:31033"
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                                                                                                                                                                                                                                                                /organism="Brugia malayi"
/strain="TRS"
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1. .668
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Takifugu rubripes.
Takifugu rubripes
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435 bp. mRNA linear EST 18-APR-2002
Yonic inner ear subtracted cDNA Danio
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Actinopterygii; Neopterygii; Teleostel; Ostarlophysi; Cypriniformes
; Cyprinidae; Danio,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 435)
Colambra, R., Well, D., Brottler, P., Blanchard, S., Levi, M., Hardelin, J. P., Welssenbach, J. and Perit, C. A subtracted cDNA library from the zebrafish (Danio rerio)
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                                                                                                                                                                              Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrel@genoscope.cns.fr. Web : www.genoscope.cns.fr
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                                                                     Length 403;
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Pred. No. 3.9e+02;
0; Mismatches 29; Indels
  1 cthers
                                                                                                                Incels
                                                                                                                                                                                                                                                                                                                                                                                                     AL726759 ARNA 110ea.
AL726759 Danio rerio embryonio inner ear subtrac
rerio CDNA clone BNOAA0882F04 5', mRNA sequence.
                                                                6; DB 17;
4e+02;
ches 29;
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/dev_stage="enbryonic"
/note="subtracted tons library"
102 c 65 g 125 t
102 t
                                                                                        ed. No. 4e+07
Mismatches
                                                                  Score 31.6;
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77 TTAGATAIGTAAAF 90
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AQ899744
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JOURNAL
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                   AUTHORS
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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AL514767 LTI_NFL006_PL2 Homo sapiens cDNA clone CL0BB0152G02 3
                                                                                                                    1 (bases 1 to 555)
El-Sayed,N., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J., Fraser,C. and Adams,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Drace 1660.
                                                                                                                                                                                                    Determination of clone end sequences from Trypanosoma brucel GUTar.
                                                                                                                                                                                                                                                                                                                                                                                                         Email: nelsayedetigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA ibrary constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
Seq primer: M13-Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sheared to give a tight size distribution (approx 2 kb). The v + 1 method used for the library constrigation is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                      Trypanosoma brucei.
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                   Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="Sheared DNA-17L3"
/clone_lib="Sheared DNA"
                                                                                                                                                                                                                                           Unpublished (1999)
Other_GSSs: Sheared DNA-17L3.TF
Contact: Najib M. El-Sayed
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AQ651385.1 GI:5144571
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vector. Library was normalized. Library was constructed by Life Technologies. Context: Feng Liang Life Technologies, a division of Invircogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filangelifetech.com URL: http://fullength.invirrogen.com.
                                                                                                                                                                                                                                                                                                                                                                                /clone='CLOBB0152G02'
/clone='Li="FFL006_PL2"
/closu=_lype="placenta"
/clos="Vector: pCWVSPORT 6; Site_1: NoI!; lst strand cDNA was primed with a NoI! oligo(df) primer. Five prime end enriched, double-stranded cDNA was digested with NoI I and cloned into the NoI I and Eco RV sites of the pCWVSPORT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mahairas,G.G., Mallace,J.C., Smith,K., Swartzeil,S., Holzman,T.,
Keller,A., Shaker,R., Furlory,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS 10-NOV-1999
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Clones are derived irom the human BAC library RFCI-11. For BAC
library availability, please contact. Pieter de 50ng
(pieterédejong.med.buffalo.edu). Clones may be purchased from
BACFAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (infoéresgen.com). BAC end Web Server:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HS_5234_Al_F10_T7A RPCI-11 Hunan Male BAC Library Homo sapiens genomic clone Plate=5002 Col-19 Row-K, DNA sequence.
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BP 191 91006 EVRY cedex - France
Emali: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Proc. Natl. Acad. Sci. U.S.A. 56 (17), 9739-5744 (1959)
99380589
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Pred. No. 3.8e+62;
6; Mismatches 25; Indels 6
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 95169, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 otners
1 (bases 1 to 578)
Li,W.B., Gruber.C., Jessee,J. and Polayes,D.
Full:length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
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                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                               Location/Qualifiers
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ilarity 58.1%;
Conservative 6
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Fax: (206) 616-3887
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AW988030
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COMMENT
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                                                                                                                                                                                                                                                          /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
PBACe3.6 vector at EcoRI sites.

3. 236 c 140 g 338 t
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RPCI-23-282B4.IJ RPCI-23 Mus musculus genomic clone RPCI-23-282B4,
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: szhaoétigr.org
Clones are derived from the mouse BAC library RFCI-23. FOR BAC
Clones are derived from the mouse BAC library RFCI-23. FOR BAC
Library availability, please contact Pieter de Jong
(pleterédejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (infoéresgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6
Class: BAC ends.
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1. (bases 1 to 554)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        31.3%; Score 31.6; DB 17; Length 911; 62.8%; Pred. No. 3.7e+02;
                                                                                                                                                                           /clone="place=9002 col=19 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Dr., Rockville, MD 20850, USA
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Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                      /organism="Homo sapiens"
                                                                                   High quality sequence stop: 911.
Location/Qualifiers
http://www.htsc.washington.edu
Plate: 9002 row: K column: 19
Seq primer: T7
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Contact: Shaying 2hao
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AQ931126.1 GI:6620140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Conservative
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Fax: 301 838 0208
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                                                                     Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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/organism="Mus musculus"

/db\_xref="taxon:10090"

/strain="C57BL/6J

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AW588030 452 bp mRNA linear EST 02-JUN-2000 uf91c01.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1529472 5' similar to TR:094636 094636 HYPOTHETCAL PROTEIN;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /nac._vector.put71D-Pac (Pharmacia) with a modified polylinker; ist strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dI) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library is normalized. Library was constructed by Bento Scares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                            /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECGKI; Site_2: ECGKI; Famale C57BL/5d mouse Kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECGKI and ECGKI Methylase. Sige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (control of control 
                                                                                                                                                                                                                                                                                                                                                                                              selected DNA was cloned into the pBACe3.6 vector at the EcoRi sites. The ligation products were transformed in DH10B electrocompetent cells (BRL ife Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. M31:945572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 CICCICITGIGGIAAAGCICAIGCCTTTTTTTTCCCTTTGTAATICTITGTTTTTA 121
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Pred. No. 4.3e+02;
0; Mismatches 31; Indels 0;
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Pred. No. 4.9e+02;
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/tissue_type="mammary gland"
/lat_host="DH10B"
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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/clon=="IMAGE:1529472"
/clone="RPCI-23-282B4"
/clone_lib="RPCI-23"
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                                                                                                                                                 /lab_host="DH10B"
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                                                                                           /sex="Female"
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Search completed: December 8, 2002, 07:50:31 Jor time: 790:132 secs

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December 8, 2002, 07:10:23 ; Search time 26.6318 Seconds (without alignments) 1478.802 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                350425 seqs, 194966369 residues
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	ដូច	Se 4447, Ap	se 8767, Ap	ze 8543, Ap	se 5, Appli	5 73, Appl	ce 243, App	se 10713, A	se 2, Appli	ze 3949. Ap	se 3, Appli	se 25, Appl	se 3, Appli	se 1695, Ap	se 3, Appli	se 1, Appli	nce I, Appli	nce 1, Appli	Se 33271, A
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 3	Sequence	Seguence	Sequence	Sequence 33
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		12-4447	12-8767	42-8943	52-5	7-73	83-243	61-10713	05-2	07-3949	20-3	97-25	20-3	64-1695	12-3	07-1	668-1	686-1	61-33271
SUMMARIES	1	US-09-815-242-4447 US-09-815-242-8393	US-09-815-242-8767	15-09-815-242-89	US-10-051-952-	S-10-001-887-7	US-09-854-883-	JS-09-864-761-	S-09-791-105-2	S-09-880-107-	S-09-813-320-	15-09-751-797-25	IS-09-813-320-	JS-09-764-864-	US-09-742-312-	US-09-946-807-	US-09-795-668-	-989-561-60-SD	JS-09-864-761-332
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Score 32; DB 10; Length 288; Pred. No. 2.2;

31.78;

Query Match Best Local Similarity

ORGANISM: Staphylococcus aureus US-09-815-242-4447

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FIDE GENERALS: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT APPLICATION NUMBER: 00/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR RELICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DAIE: 2000-05-23

PRIOR FILING DAIE: 2000-05-23
                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in
TILLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DAIE: 2000-11.27
PRIOR FILING DAIE: 2000-11.27
PRIOR FILING DAIE: 2000-12-22
PRIOR PILING DAIE: 2001-12-16
PRIOR PLING DAIE: 2001-10-16
NUMBER OF SEQ ID NOS: 1410
SGCTWARE: FRANCE; FRANCE; FRANCE; FRANCE; PRIOR WINDOWS VERSION 4.0
SEQ ID NO 8767
LENGIH: 303
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001.03-21
PRICE APPLICATION NUMBER: 60/219,078
PRICE APPLICATION NUMBER: 60/206,848
PRICE FILING DATE: 2000-05-23
PRICE FILING DATE: 2000-05-23
PRICE FILING DATE: 2000-05-26
PRICE FILING DATE: 2000-05-26
PRICE APPLICATION NUMBER: 60/207,727
PRICE FILING DATE: 2000-05-26
PRICE APPLICATION NUMBER: 60/242,578
PRICE FILING DATE: 2000-10-23
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Patent No. US2020061569A1
GENERAL INFORMATION:
APFILCANT: Hasalbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyskind, Judith W. Hall, Daniel
Irawick, John D. Carr, Grant J. Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Staphylococcus aureus
Ohlsen, Karl L. ...
Zyskind, Judith W. Wall, Daniel
Trawick, John D.
                                                                                                                                                           Carr, Grant J.
Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCCATION: (1)...(303)
US-09-815-242-8767
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US-09-815-242-8943/c
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APPLICANT:
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APPLICANT:
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    0; Mismatches 20; Indels 0; Gaps
                                                                   38 AIGCTITICCIGITAGATACITICIGTICATAGATAGATAGATAGA AGONTAGA GA HILLI HILLIH HILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 AIGCCTTTTCCTGTCTTGATAATTCTTTCTTTCTTCATTAGATATGTAAATGCTTTCA 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Disen, Kari L.
APPLICANT: Disen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: 4all, Daniel
APPLICANT: Garr Grant J.
APPLICANT: Garr Grant J.
APPLICANT: Tamamanco, Robert T.
APPLICANT: Tamamanco, Robert T.
APPLICANT: Tamamanco, Robert T.
APPLICANT: Tamamanco, Robert T.
APPLICANT: Namamanco, Robert T.
CURRENT: FLING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SECONTRON NO SASE
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US-09-815-212-8767/c
Sequence 8767, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 8393, Application US/09815242; Patent No. US20020061569A1
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ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W
    Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : LOCATION: (1)...(303)
US-09-815-242-8393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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US-09-815-242-8393/c
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IILE OF INVENITON: Compositions and Methods Relating to Breast Specific Genes and FILE REFERENCE: DEX-050: DEX-
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APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Madeline M. Butler
APPLICANT: Robert McKay
IIIIE OF INVENTION: ANTISENSE MODULATION OF PIPIB EXFRESSION
IIIE OF INVENTION: ANTISENSE MODULATION OF PIPIB EXFRESSION
FILE REFERENCE: 1201-0576
CURRENT APPLICATION NUMBER: US 09/629,644
PRICR FILING DATE: 2000-07-31
PRICR PLING LOATE: 2000-07-31
PRICR PLING LOATE: 2000-01-18
NUMBER OF SEO ID NOS: 389
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                                                                                                                                                                                                                                                                    PRIOR APPLICATION UNMER: 60/249, 996
PRIOR FILING DAIE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,563
PRIOR FILING DAIE: 2000-11-22
NUMBER OF SEQ ID NOS: 137
SEQ ID NO 73
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Patent No. US20020055479al
GENERAL INFORMATION:
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OTHER INFORMATION: a, c, g or
NAME/KEY: misc_feature
LCCAIION: (245)..(246)
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COTHER INFORMATION: a, c, g or
US-10-001-887-73
   Recipon, Herve
Cafferkey, Robert
Sun, Yongming
Liu, Chenghua
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapien
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Matches 52; Conserva
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Best Local Similarity
Matches 52; Conserva
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   APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.7%; Score 32; DB 10; Length 303; 68.8%; Pred. No. 2.3; tive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10051952
Figure No. US20020107199A1
Control No. US20020107199A1
Control No. Methods of Administering Botulinum Toxin
ILLE REFERENCE: 2933CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2043 TTCTCTCTTTGAATAGAACTATAAAAGGT 2011
RIOR FILING DATE: 2000-05-26
RIOR APPLICATION NUMBER: 60/242,578
RIOR FILING DATE: 2000-10-23
RIOR FILING DATE: 2000-11-27
RIOR FILING DATE: 2000-11-27
RIOR FILING DATE: 2000-11-27
RIOR APPLICATION NUMBER: 60/257,931
RIOR APPLICATION NUMBER: 60/269,308
RIOR FILING DATE: 2001-02-16
RIOR FILING DATE: 2001-02-16
RIOR FILING DATE: 2001-02-16
RIOR FILING DATE: 2001-02-16
RIOR FILING DAIE: FOR FILING DAIE: 1001-02-16
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URRENT FILING DATE: 2002-01-17
RIOR APPLICATION NUMBER: 09/730,237
RIOR FILING DATE: 2000-12-05
UNBER OF SEC ID NOS: 12
UTBER OF SEC ID NOS: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                IYPE: DNA
ORGANISM: Staphylococcus aureus
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E.st Local Similarity 68.89
M.tches 44; Conservative
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US--9-815-242-8943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
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US- 0-051-952-5/c
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US- 0-001-887-73
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RESULT 9.

Sequence 2, Application US/09791105

Sequence 2, Application US/09791105

Patent No. US200202225A1

SERENAL INFORMATION:
APPLICANT: Epidauros Blotechnologie AG

TILLE OF INVENTION: Method for detecting the presence of at least one single allel

TILLE OF INVENTION: a deletion mutant

FILE REFERENCE: EPI 01/00

CURRENT APPLICATION NUMBER: US/09/791,105
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                                                                                                                                       10 TGGAITTTGITTTCTTTTTICATTAITTTAIGCTTCATTTTAAAAATGTAAAICTTT 69
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ITILE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE KEFRENCE: 44921-5028-WO CURRENT FILING DAIR: 2001-06-14
PRIOR REMY FILING DAIR: 2000-06-14
PRIOR FILING DAIR: 2000-06-14
PRIOR FILING DAIR: 2000-06-14
PRIOR FILING DAIR: 2000-06-14
PRIOR FILING DAIR: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTING VET. 2.1
SEQ ID NO 3949
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US-09-880-107-3949
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Pred. No. 85;
0; Mismatches 25; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 10; Length 5000;
Pred. No. 49;
0; Mismatches 25; Indels
Score 28; DB 10; Length 380;
Pred. No. 29;
0; Mismatches 20; Indels
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US-09-880-107-3949/c
Sequence 3949, Application US/09880107
Patent No. USZ0020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-02-22
PRICR APPLICATION NUMBER: EP 00103844.7
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 5000
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     27.78;
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Best Local Similarity 63.2%;
Matches 43; Conservative (
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Best Local Similarity 63.28
Matches: 43; Conservative
                                                       Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRGANISM: Homo sapiens US-09-791-105-2
       Query Match
Best Local Similarity
Matches 40; Conserv
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FROBES USEFUL FOR
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FROBES USEFUL FULL BY INTERNATION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Accordica - X - 1
CURRENT PAPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03-09
PRIOR FILING DATE: 2000-06-03-09
PRIOR PAPLICATION NUMBER: US 69/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR PAPLICATION NUMBER: GB 24263.6
       Db. 47637 CTTTGTTCTGCTGATTGATTACAGCTTGTATATATCTCCATATTTCTAAGCAAAATGIII 47596
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.97
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.95
US-09-864-761-10713
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                                                                                       Db 47697 ATCTTTTTAAATTTATAAATTCTTTTATT 47727
                                                       70 ITCTICATIAGATATGTAAAIGCTTTCAAGT 100
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00666
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APPLICATION NUMBER: PCT/USO1/00665
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/USO1/00663
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
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FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                 Sequence 10713, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
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SOFTWARE: Annomax Sequence
SEQ ID NO 10713
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ORGANISM: Homo sapiens
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US-09-864-761-10713
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APPLICANT: ZHANG, HONGYU et al.

IIILE OF INVENTION: ISOLATED HUMAN IRANSPORTER PROTEINS,

IIILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN IRANSPORTER PROTEINS,

IIILE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CLOOI172

CURRENT APPLICATION NUMBER: US/09/813,320
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1 Similarity 54.5%; Pred. No. 1.6e+02;
55; Conservative 0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 64.1%; Pred. No. 1.18-02;
Matches 41; Conservative 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792 SEGTIMARE: Patentin Ver. 2.0 SEQ ID NO 1695 ILENGIH: 21045
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US-09-764-564-1695

J Sequence 1695, Application US/09764864

Factor No. US20020132753A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TILLE CAN TOWN NUMBER: US/09/764,864

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT APPLICATION NUMBER: US/09/764,864
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                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILTING DATE: 2001-03-21 NUMBER OF SEQ ID NOS: 4 SOTTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 LENGIE: 397658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LCCATION: (1)...(397658)
OIHER INFORMATION: n = A, T, C or G
                                                                                                                                                                                            Sequence 3, Application US/09813320 Patent No. US20020142378&1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) ATPE: DNA
) ORGANISM: Homo sapiens
US-09-764-864-1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                     3118 3TT 3120
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                                          99 GIT 101
                                                                                                                                                                        US-05-813-320-3
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Best Local Si
Marches 55;
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IILE OF INVENTION: ISOLATED HUMAN TRANSPORTER FROTEINS,

IILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

IILE OF INVENTION: AND USES THEREOF

ILE REFERENCE: CL001172

CURRENT APPLICATION NUMBER: US/09/813,320

SURRENT FILING DATE: 2001-03-21

SUBRENT FILING DATE: 2001-03-21

SUBRENT FILING DATE: 2001-03-21
                      39 TGCCTTTTCCTGTCTTGATAATTCTTTCTTTCTTCATTAGATATGCAATGCTTTCAA 98
11 TGTGGTCTCCTGACTCATTAGAGCTGGCTTTTTCCTGTCTTGALAATTCTTTCTGTT 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/178,973
FRIOR FILING DATE: 1998-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/09751797; Fitent No. US20010024652A1; GINERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57HER INFORMATION: n = A,T,C or G 5.813-320-3
                                                                                                                                                                                                           S-5-813-320-3/c
Squence 3, Application US/09813320
Extenc No. US30020142378A1
GINERAL INFORMATION:
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65.1%;
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LENGTH: 4797
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US- 9-751-797-25
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RESULT 15
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US-09-742-312-3/C
is sequence 3. Application US/09742312
is patent No. US20020045166A1
is patent No. US2002004516A1
is patent No. USCOLATED HUMAN TRANSPORTER PROTEINS,
ITILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
ITILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
ITILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
ITILE OF INVENTION NUMBER: US/09/742,312
iCURRENT FILING DATE: 2000-12-22
iNUMBER OF SEQ ID NOS: 4
is SOFTWARE: FastSEQ for Windows Version 4.0
is SEQ ID NO 3
is LENGTH: 147309
is TYPE: DNA
ordANISM: Human
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	4.53	1602 Human Ill	1481 Seguence	3657 Homo sapi	498 Rat mRNA f	1297 Mus mus	3	2568 M muscu	55272 Callins G	2007	des curcus costs	4439 HOMO Sap	:1480 Sequenc	280	1382	S	AFA63658 Homo Sapi	Seguence	HOMO Sa	a sapiens	omo sable		AKU30/36 Sequence	STHEST OF	Seducino	Sednence	M.musculu	Rattus no	Mouse FI	Sednenc	Sequenc	I25171 Sequence 5	ednence	NYK/FLK-	:coturni		ednence	Danio r	5 Danio r	X83287 C.coturnix	Sedu	256 Hum	000	54	96 X	1482 S	016568 S	06405 S		
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## ALIGNMENTS

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RESULT 1 HSFLT LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL

University

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Han.H.J. Fujiwara,I., Shin,S. and Nakamura,Y.
Dinucleotide repeat polymorphism in the 3' non-coding region of the
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                                                                                                            Nucleotide sequence and expression of a novel human receptor-type tyrosine kinase gene (fit) closely related to the fms family oncogene 5 (4), 519-524 (1990)
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ILICTAYGIPOPTIKWFWHPCNHNHSEARCDFCSNNESFTLDADSNMGNRIESIIQR
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FAELVERLEDLLOANVOODGKDYIPINALIIGNSGFTYSTPAFEEDEFKESISARFY
GGSSDDVRYVNARKEMSLERIKTFEELLPNAISMEDDIGOSSILLAGFYLKFETHTD
SKFRASLKIDLRVISKSRESGLSDVSRPSFCHSSCGHVSEGKRRITYDHAELEFKIAC
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of Tokyo, 4-6-1 Shirokane-dai, Minato-ku, Tokyo 108,
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                                     2 (bases 1 to 7680)
Shibuya.M., Yamaguchi,S., Yamane,A., Ikeda,I., Tojo,A.
Matsushime,H. and Sato,M.
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Hum. Mol. Genet. 2 (12), 2204 (1993)
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Pred. No. 0;
): Mismatches
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/db_xref="taxon:9606"
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/map="13912"
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/db_xref="G1:31432"
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Homo sapiens vascular endothelial growth factor receptor (FUII)
mRNA, complete cds.
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Characterization of the VESF binding site on the Fit-1 receptor 99400442.
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/product="vascular endothelial growth factor receptor"
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/Organism="Homo sapiens"
/db_xref="taxon:9506"
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receptor: VEGF/VPF -binding; Fms/Kit/PDGF receptor family-related;
tyrosine kinase receptor.
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AGOTLFIKCRGEAAHSWSLPIIVSQEDKKLSVIRSACGRNNRQFCSTITLNMAAANHI
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Submitted (06-FEB-1994) Masabumi Shibuya, Institute of Medical
Science, University of Tokyo, Department of Internal Medicine:
4-6-1 Shirokanedai, Minato-ku, Tokyo 108, Japan (Tel:03-5449-5550,
Fax:03-5449-5425)
                                                                                                                                                                                                                                                                                                                                                              (Strain Fisher F344) adult lung and testis CDNA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
A new communication system between hepatocytes and sinusoidai endothellal cells in liver through vascular endothellal growth factor and Fit tyrosine Kinase receptor family (Fit-1 and CHONGER 1) 2683-2690 (1994)
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domain: AA759-780, tyrosine kinase domain: AA813-1152,
kinase insert region: AA930-994.*
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Neufeld,G. and Shibuya,M.
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Rat mgna for Fit-1 tyrosine kinase receptor, complete cds.
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/protein_id="Baao5857.1"
/db_xref="G1:600379"
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/dev_stage="adult"
1. 4734
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/strain="Fisher F344"
/db_xref="taxon:10116"
/clone="4-4/7-4/3-8"
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QARGWAPQIIWFKNNHKIQQEPGILLGPGNSTLFTERVTEEDEGVYRCRAINDKGVY
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WDPDEVPLDEGCERLPVDASKWEFARELKLGKSLGRGAGGRGKVVQAAREIKKSPTCR
ONLSWYKHI KEGAIASEWAALMTELKILTHIGHHUNVNLLGACTRQGPLMVIVEYCKY
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EDKSVSTVEGGEDVSEISKQPLMEDILISYSRQVARGMEFLSSRCTIREDLARRIIL
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LWEIPSLGGSPYPGVQMDEDFCSRLKEGMRMRIPEVAIPEIYQIMLDGWHKDPREPPR
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SGSSDDVPYVNARKEMSLERIKTFEELSPNATSMFEDYHLDTSSLLTSPLLKRFTWIE
TKPRASMKIDLRITSKSNEAGLSDLPGPSFCFSSGGHIRPVRQEDEDDPFLGKESCGS
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VISPNYTYLKKFPPDILIPDGORITMDSRRGFIIANATYREIGLIMCEATVNGHLYO
INYLHROTNYTLLDVQIRPPSPVRLUHGOTLVLATTELNTRVQMSWNRPGRATKR
ÄSIRORIDRSHSHNNVFHSVLKINNVESRDKGLYTCRVKSGSSEQSFNISYHVYEKGF
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Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia: Sciurognathi: Muridae; Murinae; Mus.
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/translation="MVSGMDJAVLPYALLGCLLLTGYGSGSKLKVPELSLKGTQHVMQ
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Mus musculus (strain C57BL/6J, sub_species domesticus) cDNA to
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Finnerty, H., Kelleher, K., Morris, G.E., Bean, K., Merberg, D.M., Kitz, R., Morris, J.C., Sookdeo, H., Turner, K.J. and Wood, C.R., Molecular cloning of murine FLT and FLT4 oncogene 8 (8), 2293-2298 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kondo,K., Hiratuka,S., Subbalakshmi,E., Matsushime,H. and
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ILVEKLGALLQANVQQDGKDYIPLNAILJRNSNFTYSIPIFSEDRGKDGFADPHFHSGS
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KASMKIDLRIASPRKEAGLSDLPRPSFCFSSCGHIRPVQDDESELGKESGCSPPDYN
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VKIRKOPVQETIAGRRSYRLSMEYKFAPSPETVWLKDGSPATIKSARYLUHGTSLIIK
VYTEDAODTTILLGIKQSRLFKNLDALLYWVKPOLTEKSUSBSPRLPPLGSRQV
LICTVGOTPRETTIVUMHPCHHNISKERYDFCTBNEGSTLDSSBNLGONFRESISORM
TVIEGTNKTVSTLVVADSOTPGTTSCRAFNKIKTGVTBNUKFYSTDVRGFHYSLERWP
SLEDSGTYACRANNIYTGEDILRKTEVLVRDSFAPHLLQUSTGSTSGSTTLDCQA
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Choi.K., Wall, C., Hanratty, R. and Keller, G.
Isolation of a gene encoding a novel receptor tyrosine kinase from differentiated embryonic stem cells
Oncogere 9 (4), 1261-1266 (1994)
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/protein_id="CAA55311.1"
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/cell_type="embryonic stem
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                    181 AICACTAAGGAGCACICCAICACICITAAICITACCAIGAAGGIIIGCCCIGCAAGAI 240
                                                                        2133 ICGGGCACCIAIGCGIGCAGAGCCAGGAACAIAIACACAGGGAAGACAICCIICGGAAG 2192
                                                           241 TCAGGCACCTATGCCTGCAGAGCCAGGAATGTATACACAGGGGAAGAAATCCTCCAGAAG 300
                                                                                                            2193 ACAGAAGTICTCGTTAGAGATTCGGAAGCGCCACACCTGCTTCAAAACCTCAGTGAGTAC 2252
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                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (11-JUL-2001) Masabumi Shibuya, University of Tokyo,
Institute of Medical Science; 4.6-1 Shirokane-dai. Minato-ku, Tokyo
108-8639, Japan (E-mail:shibyyafins.u-tokyo.ac.jp.
Tel:81-3-5449-5550, Fax:81-3-5449-5425)
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OTLNLTCRGEMLBGWSLPEALSKSTSKRIVNY FXACKNGTT-CST11.1.28TQANDTGR
YSCREPISEVKKRESIVVPTNDTSNPFVEMHSO FRLIFMTVGKEM1.PCRVTAPN
IAVILKKIPREILIPDGXTIIMDNMRGFRIPEATYRFIGLISCETTIGGHKYSTKVI
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I VYGIPPPKITUMMY PCRONHSKITRGECSFIDGSFILKGSNIGNRIGS IIERTAII
BORNKTRASILVVAERASSGIS COVASNIVGKABERNYSFLYDPPSGETHSLEKYPSIEG
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TCRARNIFTGKEVLOKKDVS IRAQEAPALROLMOOTVNISNSAMIEGOVHGIPEPQI
IVFKNHEELQQESGIILGPGSRMLFIERVKEEDEGLYQCAANIKGSVESTAYVIVG
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GVSRSKESGLIGIIKPRSFCSFSCDQLSESKRRYTYGNIVLEKMKACHSPPDYSSVV
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                                                                                       Yamaguchi, S., Iwata, R. and Shibuya, M. Soluble Fit-1 (soluble VECFR-1), a potent natural antiangiogenic molecule in marmals, is phylogenetically conserved in arians Biochem. Biophys. Res. Commun. 291 (3), 554-559 (2002)
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Archosauria: Aves: Neognathae: Galliformes; Phasianidae:
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/db_xref="taxon:9031"
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The transcriptional map of the common eliminated region 1 (33CER1) in 3p21.3
                                                                                                                                                                                                                                                                                                                                                                    Cn Apr 5, 2001 this sequence version replaced gi:13545633. The sequence is a consensus sequence of clone RP4-787c23 (1-140400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp
                            Kiss, H., Yang, Y., Kiss, C., Andersson, K., Klein, G., Imreh, S. and
Dumanski, J.p.
                                                                                                                                                                                                                                                              Direct Submission
Submitted (01-APR-2001) Kiss H., Microbiology and Tumorbiology
Center (MIC), Karolinska Institute, Box 280, Stockholm, S-17177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          **NOTE: This is a "working draft, sequence. It currently consists of 26 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

**Ihis sequence will be replaced

** by the finished sequence as soon as it is available and the accession number will be preserved.

** Ili32 11811: contig of 11731 bp in length

** 11812 18811: gap of 10 bp

** 25,10 25.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contig 1:
1-11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and clone RP6-188g11 (partially, 1-108303 bp). The sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone RF6-32g23 (31212-220965 bp), clone RP6-146e1 (partially,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in order and the gaps between them are represented by 100 Ns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133628-189051 bp Contig 18: 189152-189476 bp Contig 19: 189577-191375 bp Contig 18: Contig 20: 191476-201473 bp Contig 21: 201574-202307 bp
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                                                                                                                               Hum. Genet. 10 (1), 52-61 (2002)
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                                                                                                                                                                                                           REFERENCE
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Homo sapiens chromosome 3 clone RP6-32923 map 3p21.3, ***
SEQUENCING IN PROGRESS ***, 26 ordered pieces.
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primetes: Catarrhini: Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                   1434 TCITITAICTGAGAACAACGTGGTGAAGATITGTGATTTTGGCCTTGCCGGGATAITTA 1493
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                                                                                                        129384 129483: gap of 100 bp. n length 129484 131747: contig of 2264 bp in length 131742 131847; gap of 100 bp 132316: contig of 469 bp in length 132317 132416: gap of 100 bp 122417 134455: contig of 2039 bp in length
                                                                                                                                                                                                                                                                                           204979 204978: gap of 100 bp 204979 213531: contig of 8553 bp in length 213532 213631: gap of 100 bp 213532 213631: gap of 4478 bp in length
                                                                                                                                                                                                                                                                                                                                                                                      9900: gap of 100 bp
220965: contig of 1065 bp in length.
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                                                                                                                                                                                                                                   201573: gap of 100 bp 202407: contig of 734 bp in length 202407: gap of 100 bp 204878: contig of 2471 bp in length
                                                                                                                                                                                                       tp of 100 bp contig of 9998 bp in length
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Pred. No. 6.4e-268;
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ (bases 1 to 197279) [ Kaul. R. K., Olson, M. V., Zhou, Y., James, R. A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K. A., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E. D.
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Kibukawa, M., Raymond, C.
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                                                                                                                                                                                                                                                                    24655 AGIGCAAAIGGAIGASCACTICIGCAGIIGCCIGAGGGAAGGCAIGAGGAIGAGAGCIGC 24596
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                                                                                                                                                                                                      AGTACAAATGGATGAGGACTTTTGCAGTGCCTGAGGGAAGGCATGAGGATGAGATCC 1715
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AC104439.2 GI:21490240
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                                                                                 GIGGICTIACGGAGIAIIGCIGIGGGAAAICTICICCTIAGGIGGGICTCCATACCCAGG
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Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
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Saenphimmachak,C., Phelps,K.A., Buckley,D.,
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Center: University of Washington Genome Center Web size: http://www.genome.washington.edu Derating Center: unschiegel.ashington.edu Derating Center: unschiegel.ashington.edu Center Clone name: RPI1-732E15 (bc0564) Sequencing vector: plasmid; 108722; 484 freeds Center Clone name: RPI1-732E15 (bc0564) Sequencing vector: plasmid; 108722; 484 freeds Center Clone name: RPI1-732E15 (bc0564) Sequencing vector: plasmid; 108722; 484 freeds Center Rice 10727; 108722; 484 freeds Consensus guality; 107168 bases at least 030 Consensus guality; 107168 bases at least 030 Consensus guality; 107158 bases at least 030 Consensus guality; 107159 bases at least 030 Consensus guality; 10725 bases at least 030 Consensus atea charge days at least one plasmid subclone or more than one Hill Consensus det least one plasmid subclone or more than one Hill Consensus days at least one plasmid subclone or more than one Hill Consensus with sequence has been reduced by at least one plasmid subclone or more than one plasmid plasmid the base or more than			9821 9472 5477 5348	515 <800 305 <800	8587 8291 25245 25541	7446 7591 3988 4121	2088 2075 1533 1598	2509 2517 631 <800	3519 3501 90 <800	26 <800 402 <800	925 933 3350 3490	98 <800 4577 4515	6409 6410 1229 1183	1383 1376 4221 4331	. 15048 15829 3980 4121	1875 1877 2548 2497	4169 4068 574 <800	1674 1683 2332 2309	1	5227 5082 5692 5632	15464	14333 14296 608 <800	1026 1026 3930 3895			8413 8291	1376		5644 21060 2	3278 3700	3501	2738 2763 10705 10502	237 <800 3128 3317	6715 6823 183 <800	201 <800 3255 3490	1002 1026 5693 5632	227 - 1000
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1715 TGAGTACTCTACTCCTGAAATCTATCA 68048 TGAGTACTCCACTCCTGAAATCTATCA 1776 AGAAAGCCCAAGATTTGCAGAACTTGT 67988 AGAAAGGCCAAGATTTGCAGAACTTGT 1836 ACACAGGATGGTAAAGACTACATCCT 67928 ATAACAGGATGGTAAAGACTACATCCT 67928 ATAACAGGATGGTAAAGACTACATCCT 67928 ATAACAGGATGGTAAAGACTACATCCT 1896 TACATACTCAACTCCTGCCTTCTCTGA 1955 GTITAATTCAGGAAGCTCTGATGATGT 67808 GTITAATTCAGGAAGCTTTTGAAGAACT	decochackackattical interpretation i	Query Match Best Local Similarity 65.5%; Pred No. 3.8e-197; Matches 1077; Conservative 0: Mismatches 562; Indels 6; Gaps 2; Matches 1077; Conservative 0: Mismatches 562; Indels 6; Gaps 2;  QY 218 TCATGAATGTTCCTGCAGATCCAGCCCTGCCGCGAGGCCAGGAATGTATACA 277  Db 1885 ITAAGAATGCTTGCGGAGACCAAGGAGATTACTGCTTGCTT
6998         7317         431         <800	Query Match         45.4%;         Score 953.2;         DB 9;         Length 197279;           Best Local Similarity         94.5%;         Pred. No. 5.4e-267;         Local Similarity         94.5%;         Pred. No. 5.4e-267;         Antches         98;         Indels         0;         Gaps         0;           Abstches         988;         Conservative         0;         M:Smatches         58;         Indels         0;         Gaps         0;         Caps         0;         Caps         0;         Caps         0; <td>Qy         1416 CCTGGCAGCAGAAACAITCITIAACTGAGAACAACGIGGIGAAGAITIGIGAITITIGG 1475           Db         68348 CCTGGCAGCAGAAACAITCITIAACTGAGAACAATGIGGIGAAGAITIGIGAITITIGG 68289           Qy         1476 CCTIGCCCGGGAATTTAAAGAACCCCGATTATGIGAGAAAAGGAGATACTCGACTICC 1535           Db         68288 CCTIGCCCAGGAATTTAAAAACGCCGATTATGIGAGAAAAGGAGAATTTGACTICC 68229           Qy         1536 TCTGAAATGGATGATTTAACAAGAACGCGATTATGIGAGAAAAGGAGACTTGACTT</td>	Qy         1416 CCTGGCAGCAGAAACAITCITIAACTGAGAACAACGIGGIGAAGAITIGIGAITITIGG 1475           Db         68348 CCTGGCAGCAGAAACAITCITIAACTGAGAACAATGIGGIGAAGAITIGIGAITITIGG 68289           Qy         1476 CCTIGCCCGGGAATTTAAAGAACCCCGATTATGIGAGAAAAGGAGATACTCGACTICC 1535           Db         68288 CCTIGCCCAGGAATTTAAAAACGCCGATTATGIGAGAAAAGGAGAATTTGACTICC 68229           Qy         1536 TCTGAAATGGATGATTTAACAAGAACGCGATTATGIGAGAAAAGGAGACTTGACTT

2186 AGSAGGAGGAGGGCCTCTACACCTGCCAGGATGCAGTGTTCTTGGCTGTGGAAAGTGG 2245 1126 AAGACTCAGGCAIIGIAIIGAAGGAIGGGAACCGGAACCICACIAICCGCAGAGIGAGGA 2185 2485 2306 TAGGCAGGGGGGGATTGCCATGTTCTTGTGGGTACTTGTCATCATCCTAGGGACG 2365 2545 2665 2786 GGAGCAAGAGAAAIGAAITIGICCCTACAAGACCAAAĞGGGCACGAIICCGICAAGGGA 2845 458 AAGAGCCIGGAAIIAIIIIASGACCAGGAAGCAGCACCCIGIIIAIIGAAAGAGICACAG 517 637 1055 GAGGGCCICTGAIGGTGAITGIIGAATACTGCAAAIAIGGAAAICTCICCAACIACCTCA 1114 1115 AGAGCAAACGIGACIIAIITITICICAACAAGGAIGGAGCACIACACAIGGAGCCIAAGA 1174 AAGAAAAATGGAGCCAGGCCTGGAACAAGGCAAGAACCAAGACTAGATAGCGTCACCA 1234 2846 AAGACIACGIIGGAGCAAICCCIG---IGGAICIGAAAGGGGGCIIGGACAGCAICACCA 2902 AAGAGGAAGCICCIGAAGAICIGIAIAAGGACIICCIGACCIIGGAGCAICICAICIGII 3022 814 934 994 ACCIGGCAGCAGAAACAIICIIITAICIGAGAACAACGIGGIGAAGAIIIGIGAIIIIG 1474 GCCIIGCCCGGGAIAIIIAIAAGAACCCCGAIIAIGIGAGAAAAGGAGAIACICGACITC 1534 1535 CTCTGAAATGGATGGCTCCCGAATCTATCTTTGACAAAA1CTACAGCACCAAGAGGGGCG 1594 578 CAGCAIACCICACIGIICAAGGAACCICGGACAAGICIAAICIGGAGCIGAICACICIAA 638 CAIGCACCIGISIGGCIGCGACICICITCIGGCICCIAITAACCCTICITAICCGAAAAA 2486 ICCCCAGAGACCGCCIGAAGCIAGAAGCCCCIIGGCCGIGGGCCCIIIGGCCAAGAGA 698 IGAAAAGGIC---TICIICIGAAATAAAGACIGACTACCIAICAAITATAAIGGACCCAG 815 TIGCCCGGGASASATITAAACIGGGCAAAICACTIGGAAGAGGGGCTITIGGAAAAGTGG 875 IICAAGCAICAGCAIIIGGCAIIAAGAAAICACCIACGIGCCGGACIGIGGCIGIGAAAA IGCTGAAAGAGGGGGCCACGGCCAGCGAGIACAAAGCICTGAIGACTGAGCIAAAAAICT GCAGCGAAAGCTITGCGAGCTCCGGCTTTCAGGAAGATAAAAGTCTGAGTGATGTGAGG AAGAGAAGAITCTGACGGTITCTACAAGGAGGCCCATCACIAIGGAAGAICTGAIITCII 2606 935 995 2963 1235 1295 1355 3023 1415 1475 ( ŏ g g à g g ò  $\delta$ ο̈́λ qq Š ò Q οy 셤 QQ ò òγ qq g δ δž qq ò g ΟŽ g δ qq g ŏ οy

PAT 08-AUG-2001 3 3263 ICTGGICTITIGSIGITITGCTGTGGGAAATAITTTCCTTAGGTGCTTCTCCATAICCTG 3322 TGTGGTCITACGGAGIAIIGCTGIGGGAAAICTICTCCITAGGIGGGICTCCATACCCAG 1654 1555 GAGIACAAAIGGAIGAGGACIIIIGCAGICGCCIGAGGGAAGGCAIGAGGAIGAGGTC 1714 CIGAGIACTCIACICCIGAAATCIATCAGAICAIGCIGGACIGCIGGCACAGAGACCCAA 1774 3443 GICAGAGACCCACGIIIICAGAGIIGGIGGAACATTIGGGAATCTCIIGCAAGCTAAIG 3502 1885 ITAAGAATGCATCCTIGCAGGACCAAGGAGACTATGTCTGCCTTGCTCAAGACAGGAAGA 1945 2005 2055 CGGCATCIGGGAATCCCCCTCCACAGAICATGIGGTITAAAGATAATGAGACCCTIGTAG 2125 278 CAGGGGAAGAAAICCICCAGAAGAAAGAAAITACAAICAGAAGCATCAGGAAGCACCATACC 337 218 ICAIGAAIGIIICCCISCAAGAIICAGGCACCIAIGCCIGCAGAGCCAGGAAIGIAIACA 277 397 Gaps 398 AIGGIAAIGGIGICCCGASCCICAGAICACIIGGIIIAAAAACAACAACAAAAIACAAC 457 AAGAGCCIGGAAITATTITAGGACCAGGAAGCAGCACGCIGTTTATIGAAAGAGICACAG 517 1775 AAGAAAGGCCAAGAIIIGCAGAACTIGIGGAAAACTAGGTGAIIIGCIICAAGCAAAIG 1946 CCAAGAAAAGACATTGCGTGGTCAGGCACTCACAGTCTCAGAGCGTGTGGCACCACGA ICCIGCGAMACCICAGIGAICACACAGIGGCCAICAGCAGIICCACCACIITAGACIGIC ANGAGGATGAAGGTGTCTATCACTGCAAAGCCACCAACCAGAAGGGCTCTGTGGGAAAGTT CAGCATACCTCACTGTTCAAGGAACCTCGGACAAGTCTAATCTGGAGCTGATCACTCTAA 9; Length 4071; linear Indels 1 (bases 1 to 4071) Kendall,R.L., Mao,X., Thomas,K.A. and Tebben,A. Human receptor tyrosine kinase, KDR patent: US 5204011-A 1 20-MAR-2001; Query Match 34.0%; Score 713.8; DB 6; Best Local Similarity 65.5%; Pred. No. 3.8e-197; Matches 1077; Conservative 0; Mismatches 562; DNA Sequence 1 from patent US 6204011.
ARI42803. GI:15104080 982 1835 TACAACAGGATGGTAAAGACTACAT 1859 U [[[[]]]] [[]]]]]CICAGCAGGAIGGCAAAGACIACAI 3527 Socation/Qualifiers /crganism="unknown" 894 c 1026 σ Unknown. Unclassified. 1159 a AR142803 Unknown DEFINITION ACCESSION 1715 ORGANISM BASE COUNT TITLE JOURNAL 338 REFERENCE AUTHORS 228 2126 518 578 AR142803 KEYWORDS VERSION FEATURES ORIGIN Q D ö g  $\tilde{\Sigma}$ CD qq á ö gG. 5 õ CC 8 g q ö  $\delta$ qq ö 5 6

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2426 AIGHACTCCCAIIGGAIGAACAIIGIGAACGACIGCCIIAIGAIGCAAAIGGGAAI 2485
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Sequence 1 from patent US 6359115.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TIGCCCGGGAGAGTTAAACTGGGCAAATCACTTGGAAGAGGGGCTTTTGGAAAAGTGG
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                                                                                                                  875 IICAAGCAICAGCAIIIGGCAIIAAGAAAICACCIACGIGCCGGACIGIGGCTGIGAAAA
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AF053558 4071 bp mRNA linear PRI 16-MAY-1998 Homo sapiens vascular endothelial growth factor receptor 2 (KDR)
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LCARYPEKRFVPDGNRISWDSKKGFIIPSYMISTAGMYFCEAKINDESYOSIMTIVVV
VGFAIXDVVLSPSHGIELSVGEKLVLNCIARIELNVGIDFNWEYPSSKHOHKKLVNRD
LKTQSGSEMKKFLSTLTIDGVIRSDQGLYTCAASSGLMIKKNSTFVRVHEKPFVAFGS
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EEVCDPKFHYDNIAGISQYLONSKRKSRPVSVKIFEDIPLEEPEVKVIPDDDQTDSGM
VLASEELKILEDRIKLSPSFGGWPSKSRESVASEGSNQTSGYQSGYHSDDIDIIVYS
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ANTILQITCRGQRDLDWLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYK
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PPPHHIHWWOLEEECANEPSQAVSVINPYPPOJEKSIJESPUSYGTOTILINTYPEEKO
PPPHHIHWWOLEEECANEPSQAVSVINPYPCEEWRSVEDFGGGWKIEVNKNOFALIE
GKNKTVSTUVQAANVSALYKCEPPLENVGRCERVISTHYPRGFETILOPDWQPTEQES
VSLOTIVIQAANVSKLGPOLIHVGELPTPVCKNLDITMKLNNTHSKNSTNDI
LIMELKNASLQOGOSYVCLAODEKTKRHCVVRQLYVLERVAPTITGNIENQTTSIGE
SIEVSCTASGNPPPQIMWFKDNFTLVEDSGIVLKDGNRNLTIRRVRKEDBGLYTCQAG
SIEVSCTASGNPPPQIMWFKDNFTLVEDSGIVLKDGNRNLTIRRVRKEDBGLYTCQAG
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DKIAICRIVAVKMLKEGAIHSEHRALMSELKILIHIGHHLNVVNLLGACIKPGGPLMV
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Mammalia: Eutheria: Primates; Catarrhini; Hominidae: Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="vascular endothelial growth factor receptor
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                                                                                                                                                                                                                                                                                                        (bases 1 to 4071)
Yu.Y., Whitney.R.G. and Sato,J.D.
Coding region for human VEGF receptor KDR (VEGFR-2)
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Pred. No. 3.8e-197;
0; Mismatches 562;
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/note-"VEGFR-2; tyrosine kinase"
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/db_xref="taxon:9606"
/cell_type="endothelium"
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AF063658
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Copyright (c) 1993 - 2002 Compugen Ltd.
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This isolated polynucleotide codes for the Staphilicoccus aureus RNA-uspendent amidotransferase C (RetC) protein (See AN61464). It was contained from a library of clones of chromosomal DNA of Sucress in E. coll. S. eureus WOH 29 strain containing the coll. S. eureus WOH 20 strain containing the coll. S. eureus WOH 20 strain containing the coll. S. eureus MOH 20 strain containing the coll. See the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA encoding S. aureus RNA-dependent aminotransferase C - used to diagnose and treat e.g. thyroiditis, lung abscess, infective endocarditis, secretory diarrhoea, cerebral abscess, conjunctivitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endophthalmitis, preseptal and orbital celluitis and darczyocystitis), kidney and urinary tract disorders (e.g. epidiaymitis, intrarenal and perinephric abscess and toxic snock syndichme), skin disorders (e.g. impetigo, folliculitis, cutanecus abscesses, celluitis, wound infection and bacterial mostils) and bone and joint disorders (e.g. septic arthritis and stepnyelitis), to assay genetic variation and to screen for artibacterial agents.
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is if, Ri is any nucleic acid residue, and is it-1000"
                                                                                                                                                                                                                                       mmay be amended by (R1)n-Y- group, where is H or a metal, R2 is any nucleic acid residue, and n is 1-1000^{\mu}
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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970S-0044365.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polynucleotide encoding polypeptide expressed Ly Staphylococcus aureus - used e.g. to treat infections of upper and lower respiratory tract, cardiac system and gastrointestinal tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphyjococcus aureus RNA-dependent amidotransierase C (ratC) gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RatC; RNA-dependent amidotransferase C; antiblotic; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This isolated polynucleotide codes for the Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA-dependent amidotransferase C (Ratc) protein (see AAW61469). Novel ratB polypeptides of the invention (see AAW61467) way interact with ratC and/or ratA (see AAW61470) polypeptides to form ratB:ratC and ratB:ratA heterodimers or ratB:ratA:ratC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interotrimers. Such heterodimers and heterotrimers are useful in methods of the invention, particularly vaccine and drug SCreening methods, e.g. for assays of ratB antagonists useful as antibacterial agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.7%; Score 32; DB 19; Length 300; 68.8%; Pred. No. 3.1;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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ID - AAV45098 standard; DNA; 300 BP.
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970S-0037857.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-416008/36.
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                                                                                                        04-FEB-1998;
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                                                                                                                                                                                                07-FEB-1997;
28-APR-1997;
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                                          12-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                 Black MT,
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23-MAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr GG;
                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus DNA for cellular proliferation protein +1368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides for the identification and devalopment of anticiptics, comprise sequences of antisense nucleic acids -
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Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from NIPO at
ftp.xipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Irawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.7%; Score 32; DB 23; Length 303; 68.8%; Pred. No. 3.1; ive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense, ds, prokaryotic cellular proliferation gene, antibiotic, antibacterial, drug design.
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Xu HH;
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                                                                                                                                                                                           AAS5:756 standard, DNA, 303 BP.
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2000US-207727P.
2000US-242578P.
2000US-25552F.
2000US-25731P.
2001US-26308P.
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                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus
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Best Local Similarity
Matches 44; Conservat
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23-CNT-2000) 2
27-MAY-2000) 2
22-MAZ-2000) 2
98 AGTT 101
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Yamamoto RE,
                                13-FEB-2002
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The intention relates to antisense inhibitors of gecus essential to prokar other cellular proliferation, their use in identifying the essential genes. Their use in the discovery of novel antibicios, the essential genes their was in the discovery of novel antibicios. The essential genes their selections and the encoded proteins. The prokaryones used are Escherichia coll, Staphylococcus aureus, Salmonella typhi, Miebalella premotionis, also useful for the identification of potential new targets in whencion is also useful for the antisense modele acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the express proteins. The proteins can be used to screen compounds in ratical drug discovery programmes. The antisense nucleic acid sequence is also useful to screen the house of the confidence of the co
        97
                             104 AUDITHOUANIOLISTICACCATHOUSCOPTICHICASOSACAFILISAAGIOTIGCA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staph; lobocous aureus DNA for cellular proliferation protein #1442.
38 AIGCOITTICCIGICTÌGATAATTOITICTGITICATTAGATATGIAAATGCTITCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleatides for the identification and develugment of antibiatios, comprise sequences of antisense nucleic acids -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; ds. prokaryotic celiular proliferation gene;
antibilitic, antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 37; Sey ID No 8767; Silpp; English.
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                                                                                                                                                                                                                                                  RESULI 8
PASSI30/c
ID PASSSI30 standard; DNA; 303 BP.
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2000US-207727P.
2000US-242578P.
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200108-269308F.
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Yamanoto RI, Xu HH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococous aureus.
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P-PSDB: AAU37271.
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22-DEC-2000;
                                                                                                            98 A RIT 101
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text 11. They

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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable acidum, preferably selected from a floppy or hard disx, random access memory (RAM), read-only memory (ROM) or CD-ROM, Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be obtained specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a kit for the immunodatection of polypeptides can also be used in a kit for the immunodatection of standing ceilulitis, eyelld infections, food poisoning, osteomyelitis, shurding ceilulitis, eyelld infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syntome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used in the polypeptides. The new DNA sequences can be used in the polypeptides. The new DNA sequences can be used in the polypeptides. The new DNA sequences can be used in the polypeptides.
                    gruphese bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence.
                                                                                                                                                         These bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide(s) and proteins derived from Staphylococous aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homologues of any of the S.aureus DNA sequences contained on the computer readable medium.
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Pred. No. 6.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 776-784; 3271pp; English.
                                                                                                                                                         "these bases
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68.8%;
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11581..11640
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                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN
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                                                                                                                                                                                                                                                                                                                                     07-JAN-1997;
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    misc_feature
                                                                                                                    misc_feature
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ID ABQ881
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Matches
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. They
are included to maintain the nucleoride numbering
given in the specification for this DNA sequence.
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence.
conjunctivitis, osteomyelitis, skin infections and toxic shock syndrome. The present sequence is also useful for detecting Staphylococcal infections in biological samples.
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/note= "these bases represent a line of missing text in
/note= "these arearification. They
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                                                                                                                                                                                                                     Gaps.
                                                                                                                                                                                                38 AIGCCITTICCIGICITGAIAAIICITTCITTCITCATTAGAIAIGTAAAIGCITICA 97
                                                                                                                                                           0;
                                                                                                                  31.7%; Score 32; DB 21; Length 3400;
                                                                            Sequence 3400 BP; 1256 A; 510 C; 648 G; 986 T; 0.other;
                                                                                                                                      Pred. No. 5.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus contig SEQ ID #154.
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781..840
                                                                                                                                                                                                                                                                                                                                                                                                                AAV74465 standard; DNA; 13542 BP.
                                                                                                                                    68.88;
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Myers EW;

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capable of detecting 1000 or more genes from brosophila. The invention is useful in developmental biology and in elucidating cell signalling and insection interactions in higher enkaryotes for the development of disoloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed at five sequence data for this patent did not form part of the printed at five view. The abblished_pet_sequences.
                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Proscophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                               Ine invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7914 BF; 1679 A; 2004 C; 1981 G; 2250 I; 0 other;
                                                                                                                                                                                             Claim 1; SEC ID NO 7142; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: December 8, 2002, 06:02:36 Job time : 154.05 secs
                                   Li PWD,
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                                   Venter JC, Adams M,
                                                                   WPI; 2001-656860/75.
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 (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental blology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DAM sequences (ABLIGIT), expressed DAM sequences (ABLIGIT) and the encoded proteins. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30.2; DB 23; Length 4328;
Pred. No. 18;
0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 33307; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4328 BP; 1144 A; 996 C; 1077 G; 1111 T; 0 other;
                                                                                                                                                                                                              Li PWD, Myers EW;
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62.7%;
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11-JUL-2000; 2000US-0614150.
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11-JUL-2000; 2000US-0614150.
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Indels

0; Mismatches Score 30.2; 1 Pred. No. 21;

Length 7914;

DB 23; 28;

25

Run on:

December 8, 2002, 05:16:46; Search time 801.97 Seconds (without alignments).
3665.203 Million cell updates/sec US-09-778-900A-5\_COPY\_500\_600 101 1 atatgstgcctgtggtctcc......tatgtaaatgcttcaagtt 101 4109280 GenCore version 5:1.3 Copyright (c) 1993 - 2002 Compugen Ltd. tal number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues Fost-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries UM nucleic - nucleic search, using sw model IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 em\_htgo\_other:\* em\_sy:\* em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htg\_inv:\* em\_htg\_other:\* em\_htg\_pln:\* em\_htg\_rod:\* em\_htg\_mam:\* Minimum DB seq length: 0 Miximum DB seq length: 200000000 em\_htg\_vrt:\* em\_htg\_mus:\* em\_htg\_hum:\* gb\_ba:\* gb\_hrg:\* \*:wnu\_we 9b\_in:\*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

oo	Human DNA Homo sapi	atto	Mus muscu Homo sapi	us m	atti	OHO	One o	attus	Ollio	CEO SE	attus n	att	Homo sapi	OHO	Sn	Mus muscu Mus muscu	ğ	E S	uman	Homo sapi Homo sapi	acac	Homo sapi	acaca m	Rattus no	נוט ש	OMO	9	E SIN	omo sap	omo sap	artus Omo sa				03-AUG-2001 13,			Euteleostomi; Homo.	
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6817: con
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7 7656: cont
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7767
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ailen,N., Anderson,M.
Baldwin,J., Barna,N., Beckerly,K., BoguslavKly,L., Boukhgalter/B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MER3 repeat: matches 1. .193 of consensus"
46166. .46290
/note="LlNc5 repeat: matches 7756. .7525 of consensus"
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                                                                                                                                                                                                                                                    /noce="MIR repeat: matches 131. .241 of consensus" 37283. 3739
71028-12 repeat: matches 2688. .2739 of consensus" 37659. 37781
70059-12 repeat: matches 1. .125 of coffsensus"
                              32946. .33076
//note="FLAM_A repeat: matches 1. .133 of consensus"
33231. .33323
                                                                                                                                                                                                                                                                                                                                                                          39114. 35348
/note="MIR repeat: matches 4. .231 of consensus"
40010. 40203
/note="AluJo repeat: matches 86. .274 of consensus"
40286. 40581
                                                             33231. .33323
/note="M.N. repeat: matches 118...222 of consensus"
33433. .33747
                                                                                                                                                                                                                                                                                                                                               18866. 39047
Note-"MERSA repeat: matches 1. 186 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluSp_repeat: matches 1. .297 of consensus" 41033. 41330
41032. repeat: matches 1. .299 of consensus" 43786. .43571
                                                                                                                                      35242. .35605
/note="THEIB repeat: matches 1. .364 of consensus"
                                                                                                                                                                                                         36786. .36559
/note="MER20 repeat: matches 2. .169 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MER5B repeat: matches 1. 177 of consensus"
44671, 44839
                  .189 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .189 of consensus"
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46598. 46767
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HOMO Sapiens clone RP11-27H10, LOW-PASS SEQUENCE SAMPLING.
AC016311
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/note="89 copies 2 mer tt 57% conserved"
36786. 36959
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1 (bases 1 to 224450)
Birron, B., Linton, L., Nusbaum, C. and Lander, E.
Eimo saplens, clone RP11-27H10
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Pred. No. 4.5e-17;
                'note="MER5A repeat: matches 4.
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Best Local Similarity
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Submitted (24-NOV-1999) Whitehead Institute/MII Center for Genome Research, 320 Charles Street, Cambridge, MR. 02141, USA ON Apr 16, 2000 this sequence version replaced gi:6570658.

All repeats were identified using RepeatMasker.
Smit, A.F.A. & Green, P. (1996-1997)
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                                                                     \begin{array}{c} 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\ 3.025 \\
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57710
57810
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., Devid, R.D.

Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,

Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,

Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,

Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,

Falls, T., Ferraguro, D., Flagy, N., Ford, J., Foster, P., Frantz, P.,

Gabisi, A., Gao, J., Garcia, A., Garreri, Carra, M., Gill, R.,

Harris, C., Harris, K., Hath, M., Havlak, P., Hale, S., Hamilton, K.,

Harris, C., Harris, K., Hath, M., Havlak, P., Hawes, A., Harriandez, O., Hodgson, A., Hoyes, M., Bolloway, C., Hollins, B.,

Jacobson, B., Milly, S., Khan, U., Khuyet, S., Joudah, J., Kover, C.,

Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,

Lozdo, R.J., Lux, Lucler, R., Lide, C., Liu, M., Liu, M., Joudes, E.,

Manssey, E., Marhiney, E., McLed, M., Martindale, A., Martinez, E.,

Manssey, E., Marhiney, E., McLed, M., Martindale, A., Martinez, E.,

Miner, G., Miner, Z., Mitchell, T., Wontgan, M., Morris, S.,

Nordyen, N., Norbedo, R., Palor, P., Pull, L., Quilles, M., Ren, S.,

Rives, M., Rojudokan, I., Roce, A., Payton, B., Peery, J., Perez, E.,

Sutton, A., Soatek, A., Rojubokan, I., Rolles, M., Raiz, S., Savery, S., Soderyen, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,

Sutton, A., Soatek, A., Tabor, P., Tamerisa, K., Tang, E.,

Sutton, A., Soatek, A., Tabor, P., Tamerisa, K., Tang, E.,

Sutton, A., Soatek, A., Tabor, P., Tamerisa, K., Tang, E.,

Wang, S., Ward-Moore, S., Karren, R., Washigton, C., Watlington, S., Walliams, G., Williams, A., Wilson, B., Weiler, R., Weiler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length. (see http://www.hgsc.bom.tmc.edu/docs/Gembank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of §9 contags. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 55655 bases at least Q40
Consensus quality: 59929 bases at least Q30
Consensus quality: 62415 bases at least Q20
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contig of 1008 bp in length
gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: KAMN
Center clone name: CH230-69N22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 101987)
Worley, K.C.
Direct Submission
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2129:
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3337:
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Unpublished
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2230
3238
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AUTHORS TITLE JOURNAL

COMMENT

TITLE JOURNAL REFERENCE

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Submitted (14-500-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63158, USA on Jul 4, 2002 this sequence version replaced 91:20340525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mapping information for this clone was provided by Dr. John D. Wefburson, Department of Genetics, Washington University, St. Couis Wo. For additional information about the map position of this sequence, see http://genome.wasti.edu/gso
                                                                                                                                       Louis,
                                                                                                                                                                                                                                                                                                                                      Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOILUE: This sequence may not represent the entire insert of this close. It may be shorter because we only sequence overlapping close sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data. (1.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE INFORMATION:
The APDI-11 human BAC library was made from the blood of one male doncy; as described by Oscedawa.K., Noon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jony, P.J., (1996) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong VECIOR; pBACE3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The close sequenced to the right is RFII-52FI6, 2000 by oreciap. Actual start of this clone is at base position i of RFII-373H2; actual end is at base position 63477 of RFII-62PI6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The region from 20416 to 20419 is covered only by a por product
                                                                Direct Submission
Suffilted (04-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Parkway, St.
MO 53108, USA
                                                                                                                                                                                                                                                                  Direct Submission
Submissed (30-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitted (04-JUL-2002) Genome Sequencing Center, Washington easily School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center
Center code: WUGSC
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Center
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3 (bases 1 to 96559)
Waterston, R.H.
                                                                                                                                                                                       4 (bases:1 to 96559)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                     5 (bases 1 to 96559)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 (Cases 1 to 96559)
Waterstob, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAPPING INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MO 63108, USA
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AUTHORS.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens BAC clone RP11-373H2 from 2, complete sequence.
AC113610
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                                                                                                                                                                                                                                                                                                                                      95570 95655.gap of 100 bp 95570 95655.gap of 100 bp 95670 131654; contig of 35985 bp in length 131655 131754; gap of 100 bp 131755 170443; contig of 38689 bp in length.
                                                                                                                                              16956 17055; gap of 100 bp 111 length. 17056 28121: contig of 11066 bp in length. 28122 28221: gap of 100 bp 13273 bp in length. 17056 60394; gap of 100 bp 13273 bp in length 60295 60394; gap of 100 bp 100
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                                                                                                                                                                                                                                                                                      ip of 100 bp contig of 35175 bp in length
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Abbott,S., Haakenson,W. and Creason,K.
The sequence of Homo sapiens BAC clone RP11-373H2
Upublished (2001)
                              of 100 bp contig of 6564 bp in length
                                                                                           7: gap of 100 bp
16955: contig of 9238 bp in length
contig of 953 bp in length
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131755, .170443
/note="assembly_fragment"
a 32488 c 32968 g 49630 t
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/note="assembly_fragment"
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95670. 131654
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/db_xref="taxon:10050"
/clone="RP24-472H5"
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                       3: gap of 7617: con
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Alsbrooks,S.L., Amaratunge,H.C., Are,J.K., Eyele,M., Banks,T., Barbaroks,J., Banton,J., Binage,K., Blankenbirg,K., Bonnin,D., Buskey,J., Borles,M., Briew,M., Brown,E., Brown,M., Bryant,N.P., Burket,C., Burrell,K.L., Bryant,N.P., Bulket,C., Burrell,K.L., Bryant,N.P., Chango,C., Change,C., Chango,C., Changez,D., Chang,C., Chang,C.J., Changez,D., Chang,C., Darlor,R., David,R., David,M., David,R., J., Earnatt,C., Edgar,D., Edwards,C., Chin, H.H., Dugan-Rocha,S., Durpin, K.J., Earnatt,C., Edgar,D., Edwards,C., Chang, Y., Dinh, H.H., Gao,J., Garcla,A., Garcla, N., Gall,R., Gao,J., Garcla,A., Garcla, N., Gall,R., Gao,J., Harris, G., Harris,K., Harr,M., Havlak,P., Haves,A., Henandez,J., Harris,C., Harris,K., Harr,M., Havlak,P., Haves,A., Henandez,J., Harris,C., Harris,K., Marrin,R., Hollys,S., Carles,G., Marrines,B., Johnson,R., Marrindel,J., Lu,X., Lux,X., Landry,N., Leal,R., Gao,J., Marrinez,E., Marbaris,M., Mapus,P., Marrin,R., Marring,R., Marring
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Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
Submitted (31-JUL-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 23, 2002 this sequence version replaced gi:21914537.
Genome Center
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Worley, K.C.
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Rattus norvegicus clone CH230-6D13, *** SEQUENCING IN PROGRESS ***,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinse,
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Muzny,D.M., Adams,C., Adio-Cduola,B., Ali-osman,F.R., Allen,C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the places is not known and their order in this sequence record is
                                                                                                                                                  Sequencing vector: plasmid; 100% of reads Chemistry: Dye-primer ET: 0% of reads Chemistry: Dye-primer ET: 0% of reads Assembly program: Phrap; version 0.990315 Consensus quality: 171032 bases at least 040 Consensus quality: 171208 bases at least 020 Consensus quality: 171308 bases at least 020 Insert size: 128000; agarose-fp Insert size: 17876; aum.of-contigs Quality coverage: 12.05 in 020 bases; sum-of-contigs Quality coverage: 12.05 in 020 bases; sum-of-contigs
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36356: gap of unknown length
57 92836: contig of 56480 bp in length
7 92936: gap of unknown length
87 172076: contig of 75440 bp in length.
Location/Qualifiers
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                                                                                               Sequencing vector: M13; 0%
            Project Information ----
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/note="assembly_name:Contig29"
92937. 172076
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36357. .92836
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                                      Center project name: M_BB0157P05
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1. 36256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Conservative
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Rattus norvegicus
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AC094998
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KEYWORDS
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\* NOIE: Estimated insert size may differ from sequence length . \* (see http://www.hgsc.bom.tmc.edu/docs/Gennank\_draft\_data.html). \* NOIE: This is a "working draft' sequence. It currently

Source FEATURES Salten, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barnan, N., Bastlen, V., Bloom, L., Boyusiavky, L., Bnown, A., Camarata, J., Campophano, A., Chagoria, Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Co Estate, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Batten, W., Batten, V., Bloom, T., Boyaslavky, L., Bouhhgaller, B., Linton, L., Nusbaum, C., Lander, E., Boyaslavky, L., Chompel, Y., Canarata, J., Campoplano, A., Chang, J., Chararo, B., Choopel, Y., Canarate, J., Canapoplano, A., Chang, J., Cooke, P., DeArellano, K., Dewar, K., Dilaz, J.S., Dodge, S., Faro, S., Ferreits, P., Fitchugh, W., Gage, D., Galagan, J., Gadyna, S., Gorde, S., Goyette, M., Graham, L., Grand-Pierre, N., Cardyna, S., Gordes, Goyette, M., Graham, L., Grand-Pierre, N., Cardyna, S., Hagos, B., Horton, L., Hulme, W., Illev, I., Jonnson, R., Jones, C., Landers, T., Lehoczky, J., Levine, R., Lindblad, Toh, K., Liu, G., Machen, C., MacMan, P., McGarthy, M., McGwan, P., Marquis, N., Matchers, C., MacMan, P., Marquis, J., Marchers, C., MacMan, P., Marquis, J., Marchers, C., McGarthy, M., McGwan, P., Marquis, J., Nague, C., Nocel, S., Modyn, C., Norman, C.H., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., Connor, T., Woldman, M., Ribe, K., Rise, C., Rogor, P., Senama, J., Royen, C., Rade, M., Trigillo, J., Vassillev, H., Vo, A., Wilson, B., Wu, M., Trigillo, J., Vassillev, H., Valler, M., Viel, R., Wand, M., Travers, M Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, S., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Jones, C., Kanc, L., Kartas, A., Lehcczky, J., Lieu, C., Locke, K., Macdonald, P., Marduis, N., McEwan, P., McGurk, A., McKernan, K., McLaughilin, J., Molla, M., Morris, W., Morrow, J., Mychileckyj, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Pererson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M., Wagner, A., Nicola, M., Submitted (28-JUL-1999) Whitehead Institute/MII Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Submitted (24-MAR-2002) Whitehead institute/MIF Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, 05A On Mar 24, 2002 this sequence version replaced 91:18640683. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) Direct Submission Direct Submission TITLE JOURNAL TITLE JOURNAL REFERENCE AUTHORS JOURNAL KEFERENCE AUTHORS COMMENT

- Genome Center

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Center: Whitehead Institute/ MIT Center for Genome Research.
Center code: WIBR
                                                             Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
_______Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RP11-42F20"
/clone_lib-"RPCI-11 Human Male BAC"
344. .1086
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complement(3546, 4300)
/rpt_famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="MER2"
(721, 2337
                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens'
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family="MER2" | 1280)
281 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 | 151 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family_cu___2901)
complement(2593. .2501)
/rpt_family_*Alux*
3536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="FLAM_C" 466. .5560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(6178. .6555)
/rpt_family="LTR33A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="Charliela"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7172)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .8242)
                                                                                                                                                          Center project name: 1552
Center clone name: 42_F_20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="L2"
5233. .5328
/rpt_family="LlMC44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="AT_rich"
14642. .14673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="L1MC4a"
745. .5033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="L1MC4a"
5585. .5868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="LIPA13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="MER588"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_family="L1PAl3"
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt_family="(IA)n"
076. .5193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'rpt_family="MER58B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AluJo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="LlMC4"
[4590] ]1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'rpt_family="AluSx"
.034. .5053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'rpt_family="AluJo"
3948, .14228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="(T)n"
15048. .15355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="AluY"
                                                                                                                                                                                                                                                                                                                                                                                                 /chrcmosome="17"
/map="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (1201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (7982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement 5329
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1461. 4632
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This sequence will be replaced

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Homo sapiens chromosome 17 clone RP11-95918 map 17, WORKING DRAFT SEQUENCE, 6 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Sucmitted (06-AuG-2002) Whitehead Institute/MII Center for Gencme
Sacartes, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker.
Smit, A.F.A. & Green, P. (1956-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases I to 208010)
Birren B., Nusbaun, C., Lander, E., Ali, A., Allet, N., Anderson, S., Barra, N., Bastlen, V., Bloom, I., Boguslavkly, L., Soukhgalter, B., Comarata, J., Chang, J., Chang, J., Chazaro, B., Choepel Y., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MII Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the gaps between the submittor. provided by the submittor. Ints sequence will be replaced by the finished sequence as soon as it is available and by the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 203000, ayarose-fp
Insert size: 207310; sum-of-contigs
Quaiity covorage: 13.6 in Q20 bases; sum-of-contigs
Quaiity coverage: 13.3 in Q20 bases; sum-of-contigs
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissionsigenome.wi.mit.edu
Center: project Information
Center project name: 127508
Center clone name: 959_1_8
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1 (tasss) to 20000)
Birron, Musbeum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP11-95916
                                                                                                                                                                                                                                                                                                           HIG: HIGS_PHASE2; HIGS_DRAFT; HIGS_FULLIOP.
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by the finished sequence as soon as it is available and the accession number will be preserved.

25311: contig of 25311 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                   74: gap of 100 bp
33568: contig of 3694 bp in length
                                                                                                                        25312 25411: gap of 100 bp
25412 25839: contig of 978 bp in length
26590 26489: gap of 100 bp
26490 227297: contig of 808 bp in length
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/clone_lib="RPC1-11 Human Male BAC"
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/note="assembly_fragment"
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81634. .126114
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126215. .159223
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/db_xref="taxon:9606"
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Db 129766 ICATCAGATATGTTCAGTTTGTGAAGAT 129739

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Barran, N., Bastlen, V., Boyuslavkly, L., Boukhyalter, B., Hrown, A., Campoplano, A., Chang, J., Choegel, Y., Colangelo, M., Callins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodges, S., Faro, S., Ferrelra, P., Itthugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kartas, A., Lakoque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, K., Liu, G., MacLear, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., MacLear, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., MacCear, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., Matthews, C., McCarthy, M., Matthews, C., McCarthy, M., Mardis, M., Matthews, C., McCarthy, M., Matthews, C., McCarthy, M., Mullova, I., Menga, V., Murphy, T., Naylor, J., Najlor, J., Milovar, J., Milovar, J., Manda, V., Marthy, M., Politra, V., Kaymond, C., Peterson, K., Phulkhang, P., Pierre, N., Politra, V., Raymond, C., Peterson, K., Phulkhang, P., Pierre, N., Politra, V., Raymond, C., Peterson, K., Phulkhang, P., Pierre, N., Politra, V., Raymond, C., Peterson, K., Phulkhang, P., Pierre, N., Politra, V., Raymond, C., Peterson, K., Phulkhang, P., Pierre, N., Politra, V., Raymond, C., Peterson, K., Phulkhang, P., Pierre, N., Politra, V., Raymond, C., Peterson, M., Palana, M., Palana, V., Raymond, C., Peterson, M., Palana, V., Raymond, C., Peterson, M., Palana, V., Raymond, C., Peterson, M., Palana, M., Palana, M., Palana, V., Raymond, C., Peterson, M., Palana, M., Palana, M., Palana, V., Raymond, C., Peterson, M., Palana,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOLO SEPIENS Chromosome 17 clone RPII-95918 map 17, LOW-PASS SEQUENCE SAMPLING. ACOSTOGOS ACOSTOGOS ACOSTOGOS IN 113446320 HIGS HILS BURNAL SERVINGE ACOSTOGOS IN 113446320
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.
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1. (bases 1 to 85.1).

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 17, clone RFII-95518
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Submitted (25-MAR-2001) Whitehead Institute/MII Center for Genome Research, 320 Charles Street, Cambridge, MA 52141, USA
All reposts were identified using RepeatMasKer:
Smlt, A.F.A. & Green, P. (1996-1997)
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Web site: http://www-seq.wi.mit.edu
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\* NOTE: This record contains 10 individual

FEATURES

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BCuck, J., BOwle, S., Brleva, M., Brown, E., Brown, M., Bryant, N.P., Bunay, C., Burco, P., Burkett, C., Burrell K.L., Byrd, N.C.,
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1777: gap of unknown length
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Contact: hgsc-help@bom.tmc.edu
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Center clone name: CH230-452A23
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2 (bases 1 to 119207)
Worley, K.C.
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JOURNAL
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TITLE
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Rattus norvegicus clone CH230-452A23, *** SEQUENCING IN PROGRESS
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Muricae;
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consists of 14 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.7%; Score 34; DB 2; Length 319378; 63.4%; Pred, No. 17; cive 0; Mismarches 30; Indels 0;
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7: contig of 4490 bp in length
7: contig of 4490 bp in length
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8: contig of 8953 bp in length
8: contig of 10815 bp in length
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163391: gap of unknown length
319378: contig of 155987 bp in length.
                                                                                                                                                                 contig of 2396 bp in length.
gap of unknown length
contig of 3883 bp in length
gap of unknown length
contig of 5218 bp in length
gap of unknown length
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* (see http://www.lgsc.bcm.tmc.edu/docs/denoank_draft_data.html).

* NOTE: This is a 'working draft' sequence. ir currently
* consists of 34 configs. The true order of the pieces
* is not known and their order in this sequence record is
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Chemistry: Dye-terminator Blg Dye: 100% of reads
Assembly program: Phrap; version 0.590325
Consensus quality: 80432 bases at least 040
Consensus quality: 83768 bases at least 040
Consensus quality: 85890 bases at least 020
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ENEME OF

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DD 48296 CICCIGIICCCIGAACAIGGGATAICCITICATCTITIGGATATTIILCAGIIICLITC 48355
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                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgs.bom.tmc.edu/docs/Goebank_draft_data.html).
NOTE: This is a "vorking draft' sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                      Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA, glosses 1 to 125703)
Worley K.C.
Direct Submission
                                                                                                                                                                                   Sequencing vector: Plasmid
Sequencing vector: Plasmid
Assembly program: Phrap; version 0.990325
Consensus quality: 81420 bases at least 040
Consensus quality: 91427 bases at least 030
Consensus quality: 96014 bases at least 030
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Contact: hgsc-help@bcm.tmc.edu
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######################################		RESULT 1 BAT62725 LOCUS LOCUS LOCUS LOCUS LOCUS DEFINITION 603048450F1 NIH_MSC_1 ACCESSION BAT62725.1 GI:157542 KEYWOODS EST human. CRGANISM Homo sapiens CRGANISM Homo sapiens ELNATYOLA: Manmalla: ELLHACIA: PATHONS NIH-MSC http://myc.nc ITILE National 1 to 336) AUTHONS NIH-MSC http://myc.nc ITILE National 1 to 336) AUTHONS NIH-MSC http://myc.nc ITILE National 1 to 336) CCCMMENT Contact: Robert Strau COMMENT CONTACT STRAU CONTACT STRAUTS COMMENT CONTACT STRAU CONTACT STRAUTS COMMENT CONTACT STRAUTS COMENT CONTACT STRAUTS
GenCore version 5.1.  Copyright (c) 1993 - 2002 Comp  : nucleic - nucleic search, using sw model  on: December 8, 2002, 05:54:07 ; Sea (witho 2086.0  : ie:	### 10154066 seqs, 8097743376 residues  ###################################	71137 - CC

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Sawai, J., Shiragawa, A., Shibata, K., Yoshico M., Itoh, M., Ishli, Y., Aradawa, T., Hara, A., Fukunishi, Y., Koro, H., Adachi, J., Fukuda, S., Alzawa, M., Ishli, Y., Koro, H., Adachi, J., Fukuda, S., Shizawa, M., Sawa, H., Kidobari, T., Sodora, M., Sanda, H., Salto, R., Kadora, K., Marsuda, H., Ashburner, M., Baraicr, S., Casavant, T., Flestschand, M., Gasterland, T., Gisslo, C., Kidy, B., Kochiwa, H., Kuehl, P., Leris, S., Marsuo, Y., Nikaido, F., Escle, S., Kochiwa, H., Kuehl, P., Leris, S., Marsuo, Y., Nikaido, F., Escle, S., Tomita, M., Magner, L., Mashio, T., Sakai, K., Okido, I., Firio, M., Aono, H., Gardinol, P., de Bonaldo, M.F., Brownstein, M. J., Boll, C., Flecher, C., Fujita, M., Gariboldi, M., Ostincich, S., Hill, D., Hoffmann, M., Hume, D.A., Kanlya, M., Lee, M. H., Lycas, P., Nordone, P., Ringwald, M., Rodriquez, I., Sakanolo, N., Sasaki, H., Sato, K., Schobach, C., Seya, T., Shibata, T., Storck, K.F., Suzuki, H., Suzuki, B., Winshaw, Dorle, M., Mangari, M., Hassgawa, Y., Kewaji, H., Kohtsuki, S., And Haysshizaki, Y., Yoshida, K., Hassgawa, Y., Kewaji, H., Kohtsuki, S., And Haysshizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci,P., Shibata,Y., Hayatsu,N., Sugakara,Y., Shibata,K., itoh,W., Konno,H., Okazaki,Y., Muramatsu,M. ard Hayashizaki,Y. Normalization and subtraction of cap-trapper-seiected obnas to prepare full-length CDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Sonno,H., Akiyama,J., Nishi,K., Kitsunai,I., Tashiro,H., Itoh,M., Sumi,N., Ishili,Y., Nakamura,S., Harama,M., Mishine,T., Harada,A., Yamanoto,R., Matsumoto,H., Sakaguchi,S., Ikagami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Iogawa,Y., Izawa,M., Ghara,E., Matchiki,M., Yoneda,Y., Ishikwa,T., Ozawa,K., Tanaka,I., Matsunra,S., Kawai,J., Gazaki,Y., Nuramatsu,M., Inoue,Y., Nira, A. and Hayshizaki,Y. Riken integrated sequence analysis (RiSA) system-384-format sequencing pipeline with 384 multicapillary sequencer.
                                                                          HTC 19-JAN-2002
                                                                AXO04721

Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200012B22:FMS-like tyrosine kinase 1, full insert
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Mammalla, Eutheria, Rodentia, Sciurognatni, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                      Mus musculus (strain:C57BL/63) adult male lung cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cEAR library
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Meth. Enzymol. 303, 19-44 (1599)
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                                                                                                                                                                                                                     A126556
mino9f03.y1 Stratagene mouse diaphragm (*937303) Mus musculus cDNA clone IMAGE:521021 5' similar to gp:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN): gb:107297 Mus musculus receptor tyrosine kinase (MOUSE);, mkNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
/lab_host="sour (kanamycin resistant)"
/note="forgan: diaphragun; Vector: pBluescript SK-; Site_1:
EcoR1: Site_2: Xhol; Cloned unidirectionally from mRNA
prepared from diaphragm muscle. Primer: Oligo dI. Average
insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGGAGGAG 3' -3' adaptor sequence: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,I.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosucmi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available foyalty-free through LINL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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/clone="IMAGE:521021"
/clone_lib="Stratagene mouse diaphragm (*537303)"
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                                126 CCAAGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGG 180
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4444 Forest Park Parkway, Box 8501, St. Louis, MG 63108
Tel: 314 286 1800
Fax: 314 286 1810
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89.6%; Pred. No. 2e-18;
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Contact: Marra M/Mouse EST Project
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/organism="Mus musculus"
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Location/Qualifiers
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/clone_lib="HT0452"
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Fax: +55-11-2707001
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                                                                                                      CNSO4EJU 888.bp DNA linear GSS 21-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
104B12 of library G from Tetraodon nigroviridis, genomic survey
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Terracion nigroviridis genome. For more information, please take a look at http://www.genoscope.coms.fr/Tetracion.
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                                                                                                                                                                                                                                                                                                                                                                                                                Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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1 (bases Lto 88)

1 (bases Lto 88)

Secst-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Mincker, P., Brottler, P., Quetler, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Welssenbach, J. Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigrovíridis
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-hns 32; Indels
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/db_xraf="taxon:99883"
/clone="104812"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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339 GTGGCGAACGGGA 327
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the folicwing URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=FM1-HT0452-070 900-010-c02st3=2000-09-07st4=1)
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//dev_stage="Adult"
//dev_stage="Adult"
Site_2: Smal; A mini-library was made by cloning products
derived from ORESIES PK (U.S. Letters Patent application
NO. 196,716 - Ludrig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and obbA, amplification were performed under
                                                                                               Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Coldman, G.H., Carvalho, A.F., Matsakuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivera, P.S., Bucher, P., Jörgeneel, C. V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., Ge Souza, S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludvig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01503-010, Sao Paulo-SP,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 623)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
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BG461750 באה 11 באהליב המפוקבה באראבר מהלה אמר מהקוו 11 מיטיט מקומה 11 מיטיט מקומה 11 מיטיט מקומה 11 מיטיט מקומ
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                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3451-3456 (2000)
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80.5%; Pred. No. 6e-13;
tive 0; Mismatches 22;
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162 c 132 g 163 t
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/db_xref="taxon:9606"
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High quality sequence start: 18
High quality sequence scop: 575.
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/note="Vactor: pI-Adv; A subtraction cDNA library was constructed from E8.5 mouse craniotacial mRNA subtracted from E1.5 mouse craniotacial mRNA."

1 105 c. 128 g. 114 t.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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EST sequences from E8.5 mouse craniofacial cDNA library
Unpublished (2000)
Contact: Yoshiniko Yamada
Craniofacial Developmental Biology and Regeneration Branch
Mational Institute of Dental and Craniofacial Research
9000 Rockville Pike, Building 30, Room 405, NIDGR, WIH, Bethesda,
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                                                                                                                                                                       69 CICGACTICCTCTGAAATGGATGGCTCCTGAATCTATGTTTGACAAAATCTACAGCACCA 128
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                                                                                                                                                                                                                                                  Score 75.2; DB 13; Length 689;
Pred. No. 3.9e-12;
0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                              129 AGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGG 180
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                171 t
(Wellcome/CRC Institute).
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                167 g
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79.5%;
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Fax: 301 402 0897
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RESULT 13 66577273

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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Ronno, H., Kouda, M., W., KOya, S., Matsuyama, T., Miyazaki, A., Nomica, K., Olno, M., Okozaki, Y., Okido, T., Sato, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, I., Soqabe, Y., Suzuki, H., Iagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno.H., Eukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-resignsc.riken.go.jp,
URL:http://genome.gosc.riken.go.jp,
URL:http://genome.gosc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,W., Sugañara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNs ibraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,I., Ozawa,K., Tanaka,I., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, KIKEN Genomic Sciences Center(GSC), Yokohama Institute and Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehlro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                      Eukāryota; Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BB577273 RIKEN full-length enriched, 14 days embryo thymus Mus musculus CDNA clone 6130401C07 57, mRNA sequence.
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Contact: Yoshihide Hayashizaki
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/dev_stage="14 days embryo"
/lab_host="DH108"
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/strain="C57BL/6J"
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Location/Qualifiers
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Fax: 81-45-503-9216
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
                   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Length DB	DB	ID	Description
	74.6	24.8	5406	101	US-09-919-408-5.	Sequence : Appli
2	74.6	24.8	5406	10	US-09-872-136-5	. 43
е	74.6	24.8	5470	10	US-09-766-678-1	Sequence Appli
₹*	67.2	22.3	3120	10	US-09-982-610-22	Seguence Co Anni
'n	67.2	22.3	3501	10	US-09-919-408-3	Sequence 3 App)
φ	67.2	22.3	3501	10	US-09-872-136-3	Sequence : annii
7	65.6	21.8	4425	10	US-09-982-610-31	Code ( eochannes
ဆ	65.6	21.8	6827	10	US-09-982-610-17	
ĠΛ	65.6	21.8	9108	10	US-09-982-610-45	Sequence 25 April
10	65.4	21.7	3321	10	US-09-866-510-21	-
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13	64.8	21.5	3270	10	US-09-866~510-1	Sequence Appli
14	64.8	21.5	3270	10	US-09-866-510-3	
15	64.8	21.5	3270	10	US-09-866-510-5	167
16	64.8	21.5	3270	10	US-09-866-510-7	Sequence Appli
17	64.8	21.5	3270	10	US-09-866-510-9	Sequence 9 Appli
CO [T]	64.8	21.5	4054	σ	US-09-955-363-35	Sequence 35, Appl
<u>ه</u>	64.8	21.5	6378	10	US-09-919-497-40	Secretary Appropriate

Sequence 13, Appli Sequence 15, Appl Sequence 17, Appl Sequence 19, Appl Sequence 103, Appl Sequence 10878, A Sequence 10878, A Sequence 10873, Ap Sequence 11442, A Sequence 11442, A Sequence 203, Appl Sequence 271, Appl Sequence 273, Appl Sequence 1599, Appl Sequence 1599, Appl Sequence 177, Appl	EM CELL
US-09-769-987-1 US-09-866-510-15 US-09-866-510-17 US-09-866-510-17 US-09-866-510-17 US-09-866-510-17 US-09-960-152-10878 US-09-960-152-126878 US-09-960-152-126878 US-09-960-152-126878 US-09-960-152-10423 US-09-960-152-10423 US-09-960-152-10423 US-09-960-152-10423 US-09-964-156-1599 US-09-964-156-1599 US-09-919-1456-1599 US-09-919-1456-1599 US-09-919-1456-1599 US-09-919-1456-1599 US-09-919-1456-1599 US-09-919-1456-1599 US-09-919-1456-1599 US-09-919-1456-1599 US-09-919-1488-1799 US-09-919-1488-1797 US-09-919-1488-1797 US-09-919-1488-1797 US-09-919-1488-1797 US-09-919-1488-1798-1788-1788-1788-1788-1788-1788-17	ALIGNMENTS  19408  hor R.  IPPOIENT HEMATOPOIEIIC SI  EPIORS AND THEIR LIGAMDS  Systems Incorporated  Street  Comparible  Manage 1.0, Version = A.  A. (20/919,408  A. (20/97),451  OWN >  1.07/97,451  OWN >  1.08 PCT/US92/05401  N.1992  1.08 PCT/US92/02750  1.08 PCT/US92/02750  1.08 PCT/US92/02750  1.08 OT/906  1.09 PCT/US92/02750  1.08 OT/908  1.09 PCT/US92/02750  1.08 OT/908  1.09 PCT/US92/02750  1.08 OT/908  1.09 OT/93,065  1.08 OT/793,065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 CICGACTICCICIGAAAIGGAIGGCICCIGAAICIAICITIGACAAAAICIACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsai, Siao Ping
Mood, William I.
TITLE OF INVENTOR: PROPEIN TYROSINE KINASE AGONISI ANTIBODIES
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3533 SAGGGATGTGTGTTTTGGTGTTGCTCTGGGAAATATTTTCCTTAGGT 3585
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Indels
                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/09/766,678
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 74.6; DB 10;
Pred. No. 1.8e-13;
                  CCRRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 7683-060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEB: Genentech, Inc.
STREET: 460 Point San Brunc Blvd
CITY: South San Francisco
                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/193,829
FILING DATE: 09-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 286..4386
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/09982610 Patent N: US20020146420A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee, James M.
Matthews, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5470 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArPLICANT: Genentech, Inc.
Bennett, Brian D.
Goeddel, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212)869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.8%;
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                              ZIP: 10036-2711
CCMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown MCLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 78.88
Matches 89; Conservative
                                                                                                       STATE: New York COUNTRY: U.S.A.
                                                                                  CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-09-982-010-22
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54 TIGCCCICTICTAGACTCGACTTCCTCTGAAATGGATGGCICCTGAATCTATCATTGACA 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2588 GCAICTACACCATTAAGAGTGATGTCTGGTCATATGGAATATTACTGTGGGGAAATCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 67.2; DB 10; Length 3120;
Pred. No. 2.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lemischka, Thor R.
TILLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC SIEM CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
COMPUTER: U.S.A.
ZIP: 1010 YOUR
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPPETER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM IYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE; ImClone Systems Incorporated SIREET: 180 Varick Street CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0821P3PCI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,610
FILING DAIE: 17-Oct-2001
CLASSIFICATION: <a href="https://docs.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.nlm.ncbi.n
                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) SEQUENCE DESCRIPTION: SEQ ID NO: 22: US-09-982-610-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/446,648
FILING DATE: 1956-MAY-23
APPLICATION NUMBER: 08/222616
FILING DATE: 04.APR-1594
AIJORNEY/AGGNT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09919408; Patent No. US20020072077A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [ELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3120 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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3251 COCGGCIGCCCCIGAAGTGGATGGCCCCTGAAAGCATCTTCGACAAGGIGTACACCACGC 3310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 CICGACIICCICTGAAAIGGAIGGCICCIGAAICTAICIIIGACAAAAICTACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                    Isai, Siao Ping
Wood, William I.
TIILE OF INVENTOR: PROTEIN TYROSINE KINASE AGONISI ANTIBODIES
NUMBER OF SEQUENCES: 45
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                                            2493 AGAGIGACGIGIGGACCTTTGGGGIGCITCTCTGGGAGAICTICICICIGGG 2442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 AGAGCGACGIGIGGICITACGGAGTATIGCIGGGAAATCITCICCIIAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0821P3PCT
TELECOMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PCT-DOS/MS-DOS
SOTIWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,610
FILING DATE: 17-Oct-2001
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-962-610-17
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APPLICATION NUMBER: 08/446,648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1996-MAY-23
APPLICATION UNYBRE: 08/222616
FILING DATE: 04-APR-1594
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                              Sequence 17, Application US/09982610 Patent No. US20020146420A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          Lee, James M.
Matthews, William
                                                                                                                                                                                                                                                                   Genentech, Inc.
Bennett, Brian D.
Goeddel, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              APPLICANI: Genentech,
                                                                                                                                                    RESULT 8
US-09-982-610-17/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 83,
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                                                                  2645 GCATCTACACCATTAGAGIGATGTCTGGTCATATGCAATATTACTGTGGGAAAICTICT 2704
                                                                                                                            114 AAATCTACAGCACCAAGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 CTCGACTTCCTCTGAAATGGATGGCTCCTGAATCTATCTTTGACAAATCTACA3CACCA 128
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES NUMBER OF SEQUENCES: 45
    Ö:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
WEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 21.8%; Score 65.6; DB 10
Best Local Similarity 74.1%; Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/982,610
FILING DATE: 17-Oct-2001
CLASSIPICATION: CLASSIPICATION: CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/446,648
FILING DATE: 1996-MAY-23
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1954
ATTOKNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P0821P3PCT
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    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genethech, Inc.
STRRET: 460 Point San Brunc Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P01
                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/09982610; Patent No. US20020146420A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
Geoddel, David
Lee, James M.
Matthews, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 4425 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsai, Siao Ping
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83; Conservative
  Conservative
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                                                                                                                                                                                                                                                   2705 CACTIGGT 2712
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RESULT 9

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IIILE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES FILE REFRENCE: ERM-104.01 CURRENT APPLICATION NUMBER: US/09/866,510 CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KAZLAUSKAS, ANDRIUS
APPLICANT: IKUNO, YASUSHI
TITLE JE INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROFIC DISBASES
FILE REFERENCE: EBM-10A NUMBER: US/09/866,510
CURRENT APPLICATION NUMBER: US/09/866,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2565 CIGCCCGIGAAGIGGATGGCTCCTGAGACATCTTIGACAACTCTACACACACACAGAGT 2628
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75.0%; Pred. No. 1.7e-10;
tive 0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/250,747
PRIOR APPLICATION NUMBER: 60/250,747
PRIOR APPLICATION NUMBER: 60/280,103
PRIOR APPLICATION NUMBER: 60/289,103
PRIOR APPLICATION NUMBER: 60/289,103
PRIOR FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 33.
SEQ ID NO 3
LENGIR: 3270
TURNET: 3270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/250,747
PRIOR FILING DARE: 2000-12-01
PRIOR APPLICATION NUMBER: 60/289,103
PRIOR FILING DARE: 2001-05-07
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.1
SEGUID NO 5: 22
LENGIH: 3270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Sequence 5, Application US/09866510 ; Patent No. US20020111304A1
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Best Local Similarity 75.00
Matches 81; Conservative
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Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: CDS
) LOCATION: (1)..(3267)
US-05-866-510-3
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US-09-866-510-5
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NAME/KEY: CDS
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us-09-778-900a

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FILE REFERENCE: 1651.066/37-21(10298)c

CURRENT PRPLICATION NUMBER: US/05/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

LENGTH: 355

TYPE: ....
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROIIC DISEASES
FILE REFERENCE: ERM-104.01
CURRENT APPLICATION NUMBER: US/09/866,510
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/250,747
PRIOR FILING DATE: 2000-12-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
21.7%; Score 65.2; DB 10;
Best Local Similarity 74.5%; Pred. No. 4.7e-11;
Matches 82; Conservative 0; Mismatches 28;
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Pred. No. 1.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/289,103
PRIOR FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver: 2.1
LENGTH: 3270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09866510
Patent No. US20020111304A1
GENERAL INFORMATION:
APPLICANT: KAZLAUSKAS, ANDRIUS
APPLICANT: IKUNO, YASUSHI
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APPLICANT: KAZLAUSKAS, ANDRIUS
APPLICANT: IKUNO, YASUSHI
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Best Local Similarity 75.09
Matches 81; Conservative
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US-09-866-510-1
                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Bos taurus
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ó 2569 CIGCCCGIGAASIGGAIGGCICCIGAGACAICTITGACAACCICIACACACAGGAGAT 2628 74 CTICCICIGAAATGGAIGGCTCCTGAATCTATCTTTGACAAAAICTACAGGACCAAGAGC 133 Gaps Search completed: December 8, 2002, 09:25:43 Job time : 98.3682 secs

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Sequence 1, A
Sequence 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.50 CURRENT APPLICATION DAIA:
US-08-601-891-3
US-09-071-324-3
PCT-US92-05401-3
PCT-US92-09893-3
US-08-340-011-1
US-08-901-710-1
US-08-901-710-1
US-08-601-132-36
US-08-601-132-36
US-08-601-132-36
US-08-611-31-36
US-08-611-31-36
US-08-611-31-36
US-08-611-31-36
US-08-611-31-36
US-08-446-648-31
                                                                                                                     US-08-340-011-3
US-08-901-710-3
US-08-202-616-17
US-08-446-648-17
US-08-446-648-17
US-08-446-648-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/098,707A FILING DATE: 17-Jun-1996 CLASSIFICATION: <u >Unknown>
                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 19963PV IELECOMMUNICATION INFORMATION: TELEPHONE: 732/594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALISH
OPERATING SYSTEM: PC-DGS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MGLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                           Co., Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
                                                                                                                                                                                                                                           US-09-098-707A-1
: Sequence 1, Application US/09098707A
: Patent No. 6204011
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    APPLICANI: Kendall, Richard L
Thomas, Kenneth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGIH: 4071 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATFORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Merck & Co. SIREET: P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 732/594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1;
                                                                                                                                                                                                                                                                                                        Mao, Xianzhi
                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 07065-0907
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 US-09-098-707A-1
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Matches 9
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1325.635 Million cell updates/sec
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                                                                      06:02:46 ; Search time 69.6343 Seconds
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Sequence 5
Sequence 3
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Sequence 5
Sequence 5
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backilles1.seq:*
          5.1.3
Compugen Ltd.
                                                                                                                                                                                                  al number of hits satisfying chosen parameters:
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US-08-193-829B-1
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US-08-446-648-22
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US-07-977-451-5
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                                                                                                                                                                                441362 segs, 153338381 residues
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         GenCore version
Copyright (c) 1993 - 2002
                                                                                                           US-09-778-900A-3_COPY_200_500
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                           36.786 ...36959
7.00te="MRR20 repeat: matches 2. .169 of consensus"
7.00te="MRR20 repeat: matches 131. .241 of consensus"
7.00te="MIR repeat: matches 2688. .2739 of consensus"
7.00te="L2 repeat: matches 2688. .2739 of consensus"
7.00te="L2 repeat: matches 1. .125 of consensus"
7.00te="FlAM_C repeat: matches 1. .125 of consensus"
                          32946. 33076
/note="FLAM_A repeat: matches 1. .133 of consensus"
                                                              note="AluJo repeat: matches 86. .274 of consensus"
                                                                                                                                                                                                                                                                                                                                  38866. 39047
/note="MER5A repeat: matches 1. .186 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                       40286. 40581
/Aote="Alusp repeat: matches 1. .297 of consensus"
41033. 41330
41035. 41330
43786. 43971
            'note="MER5A repeat: matches 4, ,189 of consensus"
                                                                                                                                               Noote-"THEIB repeat: matches 1. 364 of consensus"
35886. 36063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="MERSB repeat: matches 1. .177 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-"MER5A repeat: matches 8. 189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                  39114. .39348
/note="MIR repeat: matches 4. .231 of consensus"
40010. .40203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5327. .45508
note="MER3 repeat: matches 1, .193 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 99.5%; Score 299.4; DB 9; Length 164519; Best Local Similarity 99.7%; Pred. No. 3.3e-78; Matches 300; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                 15886. .36063
/note="89_copies 2 mer tt 57% conserved"
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RS MUZYD, D.W. Addio-Oducia, B., Ali-Osman, F.R., Allen, C., Ali-Osman, F.R., Allen, C., Ali-Osman, F.R., Ali-Osman, F.R., Millen, C., Aliston, C.B., Millen, C., Aliston, C.B., Millen, C., Aliston, C.B., Millen, C., Burral, J., Benton, J., Bimage, K., Blankehoury, E., Bonnin, D., Burral, J., Benton, J., Bimage, K., Blankehoury, E., Bonnin, D., Burral, C., Burral, M. C., Caver, C., Carral, C., Burral, K.L., Byrd, N.C., Carron, F.K., Carrer, M., Cavacos, S.R., Chacke, J., Chavez, D., Chen, R., Chen, R., Chen, R., Chowdhry, I., Christopoulos, C., Clereland, C.D., Cox, C., Day-Carroll, L., Dedeloh, D.A., Davilar, H.B., Davilar, R.R., Devigado, O., Denn, R.L., Ding, Y., Dinh, H. H., Davis, C., Day-Carroll, L., Dedeloh, D.A., Delaney, K.R., Dedeloh, D., Elagg, N., Ford, J., Foster, P., Frantz, P., Erraduto, D., Elagg, N., Ford, J., Foster, P., Frantz, P., Garris, J., Gao, J., Garcia, A., Garcia, M., Bullak, P., Hawes, A., Hernandez, J., Harrandez, O., Hodgson, A., Holloway, C., Hollis, B., Homs, E., Howe, J., Jackson, L.E., Larday, R., Louis, C., Liu, J., Liu, W., Louise, G., Hume, J., Jackson, L.E., Larday, M., Maritin, R., Marting, E., Harris, C., Larda, E., Lu, X., Luder, R., Jolive, S., Jouish, G., Marting, E., Marting, E.
                   NA linear HTG 24-JUL-2002
*** SEQUENCING IN PROGRESS
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Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                   Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
__Mammalia; Eutheria; Rodentia; Sciurognatni; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemistry: Dye-terminator Big Dye: 100% of reads
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Consensus quality: 55655 bases at least 040
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                   DNA
noizasud
Rattus norvegicus clone CH230-69N22,
***, 59 unordered pleces.
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Sequencing vector: Plasmid;
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                                                                                                                                                                                                                          Rattus norvegicus.
                                                                                                                                                                                                                                                                    Rattus norvegicus
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                                                                                                                                                                                           HIG; HIGS PHASE1
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                                                                                                                  AC128808
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                                                                                                                                                                                                                                                            CRGANISM
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668 986 086 201 301	47572: gap of unknown 49426: contrig of 1856 4526: contrig of 1900 51426: contrig of 1900 51528: gap of unknown 52799: goontrig of 1171 52799: goontrig of 1171	2800 54476: contig 4477 54576: gap of 5913 57012: gap of 6713 57809: contig 7710 57809: contig 7800 5989: contig	9550 1370: contig of 1481 1371 61470: gap of unknown 1471 61470: gap of unknown 3285 6384: contig of 1814 6385 6686: contig of 2702 6087 66186: gap of unknown 6187 68110: contig of 1924	### 111	78074 802491 802591 823401 85014 85014 865114 865114 87006 87006	* 91785 91884; gap of unknown length. * 91885 93811: contig of 1927 bp in length. * 93812 93811: contig of 1927 bp in length. * 93812 95213: gap of unknown length. * 95214 95313: gap of unknown length. * 95214 95313: gap of unknown length.  Query Match Best Local Similarity 80.2%; pred. No. 4.3e-26; Matches 158; Conservative 0; Mismatches 38; insels 1; Gaps 1;	QY     46   AGGCCCCTTGCCCTTGTAGACTCGCTGTAAATGGATGGCTCCTGAATCTAT   105
Consensus quality: 55929 bases at least 030 Consensus quality: 62415 bases at least 020 * NOTE: Estimated insert size may differ from sequence length.  * Gee http://www.nosc.bom.tmc.edu/docs/Genbank_draft_data.html).	is a working draft sequence. It is a working draft sequence order in this sequence daps between the contigs are repreduct the exact sizes of the gaps are will be updated with the finished it is available and the accession	1003 1102: contig of 1002 bp in length 1003 1102: gap of unknown length 1103 2129: contig of 1027 bp in length 2130 2229: gap of unknown length 2230 3237: contig of 1008 bp in length 338 4784: contig of 1008 bp in length	4884: gap of unknown length 6614: contig of 1730 bp in 16714: gap of unknown length 8257: contig of 1543 bp in 18357: gap of unknown length 9401: contig of 1044 bp in 19601: contig of unknown length 10661: contig of unknown length	10761: gap of unknown length 11930: cont.19 of 1169 bp in 12030: gap of unknown length 13552: cont.19 of 1522 bp in 13652: gap of unknown length 15262: cont.19 of 1610 bp in 15562: cont.19 of 1141 bp in 16503: cont.19 of 1141 bp in 16603: gap of unknown length	17964: contig of 1361 bp in 18064: gap of unknown length 19537: contig of 1473 bp in 19637: gap of unknown length 18165: contig of 1528 bp in 21265: gap of unknown length 22924: gap of unknown length 23965: contig of 1041 bp in 24065: gap of unknown length 25710: contig of 1041 bp in 25710: contig of 1041 bp in 25510: contig of 1040 bp	27447: CONTIG OI 1337 bp in 272447: CONTIG OI 1337 bp in 28860: contig of 1613 bp in 29860: gap of unknown length 30063: gap of unknown length 3123: contig of 1060 bp in 3123: gap of unknown length 52867: contig of 1644 bp in 132967: gap of unknown length 32867: gap of unknown length	* 3470: contig of 1103 bp in length * 34071 34170: gap of unknown length * 36371 36470: gap of unknown length * 36371 36470: gap of unknown length * 37802 37901: gap of unknown length * 37802 37901: gap of unknown length * 37802 39087: contig of 1186 bp in length * 39088 40712: contig of 1186 bp in length * 40713 40812: gap of unknown length * 40713 40812: gap of unknown length * 42243 42342: gap of unknown length * 42343 43667: contig of 1430 bp in length * 434243 43667: contig of 1255 bp in length * 43667: gap of unknown length * 43667: gap of unknown length

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GENERAL INFORMATION:
APPLICANT: Dumoutier, Leure
APPLICANT: Dumoutier, Leure
APPLICANT: Louned, Jamila
APPLICANT: Louned, Jamila
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducibl
TITLE OF INVENTION: (TIFS)
ITTLE OF INVENTION: The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-10-16
PRICK APPLICATION NUMBER: US/09/178,573
PRICK FILING DATE: 1998-10-26
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3058 ILCCIGACCAICALLTAATGAGTGTGACTGTTTCTTCCTTTGATAATTGAAGCTTTGTA 3.17
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C.MPUTER: IBM PC COMPATIBLE
C.SEPATING SYSTEM: PC-DOS/MS-DOS
S.FTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMEER: US/08/144,602B
FILLING DAIE: 27-007-1993
CLASSIFICATION: 536
                                                                                                                                                                                                                 US-09-354-243B-25
| Sequence 25, Application US/09354243B
| Patent No. 6359117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/081446057
Patent No. 5641876
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NGBLOY DAVID APPLICANT: Wu, F. TITLE OF INVENTIN: RICE A NUMBER OF SEQUENS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarit, 65.19
Matches 41, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z.P: 14653
COM.VIER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLIMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.RUETH CLINION
CITY: ROCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3116 GTI 3120
                                                                                                                 3118 GIT 3120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US+09-354-243B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 GTT 101
                                                                                           99 GTT 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ 15 NO 25
LENGTH: 4797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-1:1-602B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
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APPLICANT: Dumouttier,
APPLICANT: Dumouttier,
APPLICANT: Loubled, Jamila
APPLICANTON: TITRE OF INVENTION: UNMER: US/09/419,568F
CURRENT APPLICANTON NUMBER: US/09/419,568F
PRIOR APPLICANTON NUMBER: US/09/419,588F
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.5%; Score 27.8; DB 4; Length 4597; 59.5%; Pred. No. 7.2; Live 0; Mismatches 32; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.5%; Score 27.8; DB 4; Length 4797; Best Local Similarity 65.1%; Pred. No. 7.3; Matches 41; Conservative 0; Mismarches 22; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Indels
                                                                                      COMPUTER READBLE FORM:
COMPUTER READBLE FORM:
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                          US/08/961,527
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Patent No. 6331613
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REBERENCE/DOCKET NUMBER: PB34C
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 175:
SEQUENCE CHARACIERISTICS:
  9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3718 ATAAAATTTTTTTTT 3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 ATGTAAATGCTTTCAAGTT 101
                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4597 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 59.58
Matches 47; Conservative
                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                      Rockville
                                          Maryland
                                                              USA
                                                                                    20850
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US-09-419-568F-25
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US-09-419-568F-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                              COUNTRY:
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CORRESPONDENCE ADDRESS:
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                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TATGGTGCCTGTGGTCTCCTGACTCATTAGAGCTGGATGCCTTTTCCTGTTTTTTT 61
                                                                                                                                                                                                                                                                                                              .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Substy Match 27.1%; Score 27.4; DB 4; Length 2340; est Local Similarity 57.6%; Pred. No. 8.2; Matches 49; Conservative 0; Mismatches 36; Indels 0.
                                                                                                                                                                                                                                                                          DB 1; Length 5643;
                                                                                                                                                                                                                                                                                                          27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hilman, Jonnifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil c.
APPLICANT: Guegler, Karl J.
APPLICANT: Yue, Henry
TITLE OF INVENTION: HUMAN NUCLEIC ACID METHYLASES
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chaganti, Raju S.K.
APPLICANT: Dyomin, Vadim
APPLICANT: Dalla-Fravera, Riccardo
TITLE OF INVENTION: CLONING AND USES OF BCL-8
FILE REFERENCE: 53828-A-PCT-US
CURRENT FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                        Score 27.8; DB Pred. No. 7.6; 0; Mismatches
                                          19603/10140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1188 CARGITITCICATCCITITATIT 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 CITTCTGTTTCTTCATTAGATATGT 86
NAME: TIMIAN, SUSAN J.

REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603
TELECOMMUNICATION INFORMATION:
TELEPRONE: 716-263-1636
TELEFAX: 716-263-1600
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-450-852-3
; Sequence 3, Application US/09450852
; Patent No. 6309860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09082310 Patent No. 6096526
                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 62.0%;
Matches 44; Conservative
                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: CDNA
US-08-144-602B-4
                                                                                                                                                                                                                                                                                                                                                                                                               88 AATGCTTTCAA 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: human
US-09-450-852-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3
LENGTH: 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-082-310-3/c
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20 CIGACICATTAGAGCIGGAIGCCITITCCIGICITGAIAATICITICIGITICAATTA 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFTARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENI APPLICATION DATA:
APPLICATION NUMBER: US/09/575,205
                                                                                                                                                                                           SOFIWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
IIILE OF INVENTION: HOMAN NUCLEIC ACID METHYLASES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.5%; Score 26.8; I
64.5%; Pred. No. 12;
ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: INCYTE PHARMACEUTICALS, INC 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                 CLASSIFICATION:
AITONNEY/AGENT INFCRATION:
NAME: CERRONE, MICHEL.
REGISTRATION NUMBER: 39,132
REFERRONCE/DOCKET NUMBER: pp-3520 US
FELECOMBUNICATION NUMBER: pp-3520 US
FELECOMBUNICATION (650) 855-0555
FILEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            US/09/082,310
                                                                                                                                  E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 3, Application US/09575205
Patent No. 6436683
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1894 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 64.59
Matches 40; Conservative
                                                                                                                                                                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                              Herewith
                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
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CALIFORNIA
                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: Bross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                               USA
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                                                                                                                                      MEDIUM TYPE:
                                                                                                 54304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1406 AA 1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIATE: CP
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                       0: Gaps
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                                                                                                                                                                                                                                                                                                                                 26.5%: Score 26.8; DB 4; Length 1894; 64.5%; Pred. No. 12; tive 0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 3573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 GAIGCCTITICCIGICITGAIAGITCTITCTGTTTCTTCATAGATAGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GOO, Zeren
APPLICANT: GOO, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheepard, Paul O.
APPLICANT: Sheepard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: GROWTH FACTOR HOWOLOG ZVEGF?
ITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGF?
FILE REFRENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DAIE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE PASSESSO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 26.4; DB
; Pred, No. 18;
0; Mismatches
                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/082,310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 42, Application US/09457066
; Patent No. 6432673
                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.18;
                                                                                                                                                                                                                                                                                                                          Query Watch 26.59
Best Local Similarity 64.55
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 69.2%
....hes 36, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (1049)...(2085)
JS-09-457-066-42
                                                                                                                                                                                                                                                                    ORGANISM: Mus musculus FEATURE:
CLASSIFICATION:
                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1406 AA 1405
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2813 GTTGGCTITTCTAATCTTGTTAAATATTTCTATTITTACCAAAGGTATTAA 2864

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APPLICANT: Upper, John L.

APPLICANT: Cleeson, Marie.

IIILE OF INVENTION: CYTOCHFOME P450 MONOOXYGENASE AND NADPH CYTOCHFOME P450

IIILE OF INVENTION: OXIDOREDUCIASE GENES AND PROTEINS RELAIED TO THE OMEGA

IIILE OF INVENTION: HEROXILASE COMPLEX OF CANDIDA TROPICALIS AND METHODS

IIILE OF INVENTION: HEARTHON THERETO

CURRENT APPLICATION NUMBER: US/09/302.620B

NUMBER OF SEQ ID NOS: 109

SOFTWARE: PALENTIN Ver. 2.1

SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 3291 TCTTTCAAGCTGGATGGCTGGTTCTGGATGGTCAATTCTGGGAGTTTCTTCA 3240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.1%; Score 26.4; DB 4; Length 3826;
69.2%; Pred. No. 19;
tive 0; Mismatches 16; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Covacci, Antonello
IIILE OF INVENTION: Helicobacter Pylori Cagi Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477.451
Sequence 90, Application US/09302620B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JMBER: US/08/477,451
07-JUN-1995
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COMPUTER REARBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                    GENERAL INFORMATION.
APPLICANT: Wilson, C. Ron
APPLICANT: Craft, David L.
APPLICANT: Birich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Brenner, Alfred A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-08-477-451-9/c
Sequence 9, Application US/08477451
Patent No. 5928865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MCCLUNG, Barbara G
REGISTAALION NUMBER: 33,113
REFERENCE/DCCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : TYPE: DNA
; ORGANISM: Candida tropicalis
US-09-302-6208-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 69.2
Matches 36, Conservative
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LENGIH: 5599 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                    APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
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                    Patent No. 6331420
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                                                                                                                     Gaps
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                                                                             Score 26.4; DB 2; Length 5599;
Pred. No. 20;
0; Mismatches 26; Indels 0
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                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/08477451
Satent No. 5928865
GENERAL INFORMATION:
TITLE OF INVENTION: Helicobacter Pylori Cagi Region NUMBER OF EQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: IBM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILLSG DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
IELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
            TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) US-08-477-451-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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                                                                              26.1%;
61.8%;
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                                                                                              Best Local Similarity 61.89
Matches 42; Conservative
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 single
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ZIP: 94508-2916
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STRANDEDNESS:
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RESULT 15 US-08-477-451-25/c

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Db 4717 TCTCTCAAAGGIIAGIGGGGAAITCTTITTCCTCTITTGIAAITTCTTIGGCAATGT 4658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.1%; Score 26.4; DB 2; Length 19932; Best Local Similarity 61:8%; Pred No. 27; Matches 42; Conservative 0; Mismatches 26; Indels 0;
                                                            APPLICANT: Govacci, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM_PC COMPALLAL
COMPUTER: IBM_PC COMPALLAL
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/08/477,451
FILING DAIE: 07-UNN-1995
"NOSTETCATION: 435
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Job time : 33:3657 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DAIE: 07-JUN-1995
CLASSIFICATION: 435
AIORNET/AGENT INFORMATION:
NAME: MCCIUNG, Barbara 6
FEGITERATION NUMBER: 33,113
Sequence 25, Application US/08477451
Patent No. 5928865
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
TELEFAX: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS: LENGTH: 19932 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE IYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYPE: nucleic acid
SIRANDEDNESS: single
IOPOLOGY: linear
                                                                                                                                                                                                                                                                         94608-2916
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                                                                                                                                                                                                                                                                                           637 GCIGCICIICAICGAGGICCGCGGGAGGCTCGGAGCGCGCCAGGCGGACACTCCICTCGG 746
                                                                                                                                                                                                                                                                                                                                                                         867 ACGGGCGCICAGGGCGGGGGGGGGGGGGGAACGAGGAGGAGGACGCACTCTGGCGGCGGG 926
   179 TGAGCGCGATGGGCAGGAGGAGGGCAAGGGCAAGAGGGCGCGGAG-AAAGACCCTGAAC 237
                                   23B CTGCCGGGGCCCGCGCTCCCGGGCCCGCGTCCCCACCCTCCCCACGCGCGCTCCGCCCC
                                                                                                                                                                                                                                                                                                              807 CGGGCGCCTGGCGGCGAGGATTACCCGGGGAAGTGGTTGTCICCTGGCTGGAGCCGCGAG
                                                                                                538 GGGCCACCCGCCCTCGTCGGCCCCCGCCCTCTCCGTAGCCGCAGGGAAGC-GAGCCTGG
                                                                                                                                                              567 GAGGAAGAAGAGGTAGGTGGGGAGGCGATGAGGGGTGGGGGACCCCTTGACGTCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour suppressor gene derived chemically modified sequence #73
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
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1340 GGTGTCTCCTGGCTGGAGCCGCGAGACGGGCGCTCAGGGCGCGGGGGCCGGCGGCGGCGGCA 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 CTTGGATCGGACTTTCCGCCCCTAGGGCCAGGCGGGGGGGCCTTCAGCCTTGTCCCTTCCC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 CAGITICGGGCGCCCCCAGAGCTGAGTAAGCCGGGTGGAGGGAGTCTGCAAGGAITTCC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAGCGCGATGGGCAGGAGGGGCAAGGCCAAGAGGCGCGCGGAGCAAAGACCCTGAAC 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fit gene encoding receptor type tyrosine kinase. The promoter is useful for the tissue specific expression of heterologous proteins. Vectors cong. the DNA were used to transform vascular endothelial cells, such that a protein of interest could be expressed. The ligand controlling the function of the promoter may be used as a neovascularisation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The DNA (nucleotides -229 to +8) contains a promoter for the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Promoter of human flt gene encoding receptor type\ tyrosine\ kinase useful for tissue specific expression of heterologous proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine kinase receptor; ilt gene; promoter; neovascularisation;
tissue-specific expression; heterologous protein production; ds.
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                                                                                                                                                                                                                                                        Promoter of human flt gene encoding tyrosine kinase receptor
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Pred. No. 9.5e-125;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 840 BP; 120 A; 269 C; 336 G; 115 T; 0 other;
                                                                1400 ACGAGGACGACTCTGCCGGCCGGGTTTGCCCGCGGG 1440
                                               ACGAGAGGACTCTGGCGGCCGGGTCTTTGGCCGCGGG 941
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 771..833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 10; 11pp; Japanese.
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                                                                                                                                                           AAT08550 standard; DNA; 840
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les 725; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94JP-0084526.
                                                                                                                                                                                                                           (first entry)
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P-PSDB; AAR77646.
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                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AFR-1994;
                                                                                                                                                                                                                         18-JUN-1996
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                                               501
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                                                                                                                            RESULT 2
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                                                                                                                                                                 The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific
Fragments of chemically modified genes associated with tumbur suppressor genes and oncogenes, useful in designing primers and prohes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events where disadvantageous to patients. The present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                               genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITCGGTGITITITIAGAITITICGGGATAGITIGAAGGGGTTAGGAGCGGCGGGATAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AGAGGGGGGGGGAGCAAAGACCTGAACCTGCGGGGCCGCGCCCCGGGGCCCGGGCCCGCGTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 genomic sequences derived from tumour suppressor genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.1%; Score 613; DB 22; Length 6316; llarity 78.2%; Pred. No. 6.4e-114; Conservative 0; Mismatches 205; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6316 BP; 1490 A; 255 C; 1803 G; 2768 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       itp.wipo.int/pub/published_pct_sequences.
                                                                                                                          ID No 73; 27pp; English.
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es 736; Conserv
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The invention relates to a nucleic acid comprising a sequence of at least 16 bases of a segment of chancelly pretreated bWh or games associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chanically modified DNA of genes associated with cell signalling, as well as oligonuclectides and/or PNA-oligomers for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling
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541 CCGIAGCCGCAGGGAAGCGAGCCIGGGAGGAGAAGAGGGGIAGGIGGGGAGGCGGAIGAG 600
                                                                                                                    661 AAGGITATAAATGGCCCCCCCCCCCCCCGCTGCTCATCGAGGTCCGCGGGAGGCTCGGA
                                                                                                                                     721 GOGGGCCAGGCGGACACICCICICGGCTCCICCCCGGCAGCGCGGCGGCGGCGGAGCGGG
                                                                                                                                                                                              GGGTGGGGGACCCCTTGACGTCACCAGAAGGAGGTGCCGGGGTAGGAAGTGGGCTGGGGA
                                                                                                                                                                                                                                       781 CICCGGGGCTCGGGTGCAGCGGCCAGCGGGCGCCTGGCGGCGAGGATIACCCGGGGAAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell signalling; cytosine methylation; cell signalling disease;
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                                                                                                                                                                                                                                                                                                                                                                             5172 ACGAGAGGACGGATTTISGCGGTCGGTCGTTGGTCGCGGG 5212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemically treated cell signalling DNA sequence#53.
                                                                                                                                                                                                                                                                                                                                                            ACGAGAGGACGGACTC/GGCGGCCGGGTCTTTGGCCGCGGG 941
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01-SEP-2000; 2000DE-1043826
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epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABI/O111-ABI/O602 represent chemically pre-treated genemic DNA's of genes associated with cell signalling.

Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                                                                                                                                                                                  European Patent Office.
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Sequence 6316 BP; 1490 A; 255 C; 1803 G; 2768 T; 0 other;

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        Length 6316;
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Match 65.1%; Score 613; DB 24; Local Similarity 78.2%; Pred. No. 6.4e-114; es 36; Conservative 0; Mismatches 205;
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Himman, Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Merner syndrome; astima; HDR syndrome; congenital heart defect; Steinfe-Choizen syndrome; renal disease; Preceiampsia; cardiac allograft vascular disease; recolorectal cancer; tiyroid cancer; cardiac cancer; cosophageal cancer; ds; tumour; immunostimulant; cardiant; antihilammatory; cosqulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunostimulant; cardiant; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to 224 nucleic acid sequences comprising at least in bases of a chemically pretreated gene associated with gene regulation
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5112 GGIIGTITTIGGTISGAGICGCGAGACGGGCGTTIAGGGCGCGGGGGGTCGGCGGCGGCGA 5171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, werner syndrome, astima, HDR syndrome, Saethre-Chotzen syndrome, renai disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          selected from 43 known genes (or complementary sequences). The Cremical pretreatment converts cytosine bases unmetnylated at the Frostition to uracil or another base with hybridistantic behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. In Edward to enable analysis of cytosine methylations. In second and complements (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis or the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preeclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the numan gene regulation-associated genes.
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                                                                                                              5172 ACGAGAGGAGGATITTGGCGGTCGGTCGTTGGTCGCGG
                                                                   901 ACCAGACGACGGACTCIGGCGGCCGGGTCTTTGGCCGCGGG
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2000DE-1032529.
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4872 GUSTGGGGGATTTTTTGACGTTATTAGAAGGAGGTGTCGGGGTAGGAAGTGGGTTGGGGA

GESTGGGGGACCCCTTGACGTCACCAGAAGGAGGTGCCGGGGTAGGAAGTGGGCTGGGGA

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721 GUGGGCGAGGGGGACACTCCTCTCCGCTCCTCCCGGCAGGGGGGCGGCGGCTCGGAGCGGG 781 CTCCGGGGCTCGGGTGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATTACCCGGGGAAGT 

661 AAGGITATAAATCGCCCCCCCCCCTCGGCTCTTCATCGAGGTCCGCGGGAGGCTCGGA

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                                 Length 6316;
Sequence 6316 BP; 1490 A; 255 C; 1803 G; 2768 T; 0 other;
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                                Score 613; DB 24;
Pred. No. 6.4e-114;
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78.2%;
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Human, signal transduction associated gene, cytosine methylation state, CpG island; signal transduction associated disease, solid tumour; cancer, antitumour; cytostatic; mutant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these epigenes, and a method for the dispnosis and/or therapy of genetic appropriate parameters of genes associated with signal transduction. The genomic obna one to obtained from cells or cellular components which centain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urise, cerebral-spinal fluid, tissue embedded in parafifin such as tissue from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The
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                                                                                                                      Signal transduction associated gene modified DNA #52.
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01-SEP-2000; 2000DE-1043826.
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                                                             601 GGGTGGGGGACCCCTTGACGTCACCAGAAGGAGGTGCCGGGGTAGGAAGTGGGGCTGGGGA
                 181 GCGGGAAGAGCAGGCAAGGGGAGACAGCCGGACTGCGCCTCAGTCCTCCGTGCCAAAAC
                                                   ACCGICGCGGAGGCGCGGCCTTCCCTTGGATCGGACTTTCCGCCCCTAGGGCCAGGC
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anglogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer

New nucleic acid fragments from chemically treated

WPI; 2002-500450/53.

Schacht O;

06-DEC-2001; 2001WO-EP14320 06-DEC-2000; 2000DE-1061338

W0200246454-A2. 13-JUN-2002. (EPIG-) EPIGENOMICS AG.

Claim 1; SEQ. ID NO 93; 41pp + Sequence Listing; German.

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the invention relates to a nucleic acid (1) comprising a segment of 18 bases of chemically pretreated DNA of anglogenesis-associated genes (II) faving sequences (ABQ66571-ABQ67178) or their complements. (1), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in anglogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neonated as the sequence of                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
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inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antidiabetic; antipsoriatic;

antiarteriosclerotic; ds.

Homo sapiens

Human anglogenesis associated polynuclectide SEQ ID NO 93.
Human; anglogenesis; methylation; eye disease; glaucoma; tumour;

ABQ67063 standard; DNA; 6321 BP.

ABQ67063

(first entry)

28-AUG-2002

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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with consulphite, of genes associated with tumour suppression and concepnes having a sequence taken from 506 (actually 533 since numbers 408, 458 and 560 are missing from the sequence listing) sequences (SS) and sequences complementary to (SS). The nucleic acid may be a form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG diructeotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or prognosis events which are diseases serving as basis for diagnosis and/or prognosis events which are diseases to parameters. The
                                                                                                                                                                                                                                                                                                                  533 genomic sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1624 AAAAAGGGAAAAAAAGCCIAAAAAAGCGAAACGGGGCIOCGAACCGGAGCGGGCIOGCGA 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2044 CCGARARAPAACACGARCAACACGCTCCCCTRARACTAARTTATTCGCARICTICCCAAAAA 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           542 CGTACCCGCAGGGAAGCGAGGCTGGGAGGAAGAAGAGGGTAGGTGGGGAGGCGGATGAGG 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CCGAAAAAGACACGGACACGCTCCCCTGGGACCTGAGCTGGTTCGCAGTCTTCCCAAAGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 IGCCAAGCAAGCGTCAGTTCCCCTCAGGCGCTCCAGGTTCAGTGCCTTGTGCCGAGGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 CCGICGCGGAGGCGCGGCCAGCTICCCTIGGAICGGACTITCCGCCCCTAGGGCGAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .804 CCSICGCGAAAACGCGACCAACTICCCTTAAAATCGAACTITCCGCCCTAAAACCAAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 GAGGGGGGGGAGCAAAGACCTGAACCTGCCGGGGCGCGCTCCCGGGCCGCGCGTGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                               of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6316 BP; 1474 A; 255 C; 1549 G; 3038 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                           is missing). Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.3%; Score 510.8; DB 22; 71.5%; Pred. No. 1.8e-93; live 0; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 71.5
Matches 671; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                    Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
     4752 AGTATTTTTACGCGCGTTCGGTTATTCGTTTTCGTCGTTTTTCTTTTTTT 4811
                                                                                                                                                                                                                            4932 AAGSTATAAAAICGTTTTCGTTTTCGTTGTTTTTATCGAGGIICGCGGGAGGIICGGA 4591
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                                                                                 GGGTGGGGGACCCCTTGACGTCACCAGAAGGAGGTGCCGGGGTAGGAAGTGGGCTGGGGA
                                                                                                                                                     781 CICCGGGGCTCGGGTGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATTACCCGGGGAAGT
                                                            541 CCGTAGCCGCAGGGAAGCGAGCCTGGGAAGAAGAAGAGGGTAG3TGGGGAGGCGATGAG
                                                                                                                                                                                                         GCGCGCCAGGCGGACACTCCTCTCGGCTCCTCCCCGGCAGCGGCGGCGCTCGGAGCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGAGAGGACGGACTCTGGCGGCCGGGTCTTTGGCCGCGGG 941
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ID AAS46352 standard; DNA; 6316
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2000DE-1043826.
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07-APR-2000;
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Length 6316;

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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is signalling, as well as a cytostatic, the object of the invention is signalling, as well as a lignoncleotides and/or PNA-oligoners for detecting cytosine methylations, as well as a merhod which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling
                                                                                                                      1325
                                                                                                                                                                                                                                                                                                                                          1264 TCCGAAACTCGAATACAACGACCAACGAACGCCTAACGACGAAAATTACCCGAAAAAATA 1255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemically treated cell signalling DNA sequence complementary to#53
                                                                                                   1444 AATAAAAACCCCTTAACGTCACCAAAAAAAATACCGAAATAAAAATAAAAAA
                                                                                                                                                              CGGGCCAGGCGGACACTCCTCTCGGCTCCTCCCGGCAGCGGCGGCGCGCTCGGAGCGGGG
                                                                                                                                                                                                                                         TCCGGGGCTCGGGTGCAGCGGCCAGCGGCGCCTGGCGCGCGAGGATTACCCGGGGAAGTG
602 GGTGGGGGACCCCTTGACGTCACCAGAAGGAGTGCCGGGGTAGGAAGTGGGCTGGGGAA
                                                                                662 AGGITATAAATCGCCCCCCCCCCCTCGGCTGCTCTTCATCGAGGTCCGCGGAGGCTCGGAG
                                                                                                                                                                                                                                                                                                                     842 GTTGTCTCCTGGCTGGAGCCGGGAGAGGGCGCTCAGGGCGGGGCCGGGGCCGGCGGGGCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell signalling; cytosine methylation; cell signalling disease;
cancer; tumour; cytostatic; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                        902 CGAGAGGACGGACTCTGGCGGCCGGGTCTTTGGCCGCG 939
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG.
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                          Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
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                                                                                                                                                                                                                          Length 6316;
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                                                                                                                                                           Sequence 6316 BP; 1474 A; 255 C; 1549 G; 3038 T; 0 ctner;
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genomic DNA's of genes associated with cell signailing
                                                                                                                                                                                                                    Score 510.8; DB 24;
Pred. No. 1.8e-93;
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                                                                                                                                                                                                                                                                                                                           Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; inflammilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gane associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the
                                                                                                                                                                                                                                                                                                                                                                                                                                colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sers/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by kits are provided. They are especially useful in diagnosis, and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Merner syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preeclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24; Length 6316;
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                                                                                                                                                                                                                                                                             Human gene regulation-associated gene oligonucleotide #126.
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1144 CGAAAAAACGAACTCTAACGACCGAATCGTTAACCCCC 1107
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ID AAS61171 standard; DNA; 6316
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2000DE-1032529.
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1624 AAAAACGGAAACAAAAACCTAAACCTAACGAAACCGCACTCCGGAACCGGAACCGGGGCGCA 1565
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  1864 CGAAAAAAACAAACAAAAAAAAAACAACCGAACTACGCCTCAATCCTCCGTACCAAAAAA 1805
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                                                                                                                                                                                                                                                             421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           662 AGGITALAAAICGCCCCCCCCCCCCCCCCCCTCTCAICGAGGICCGCGGAGGCICGGAG 721
                                                       242 CCGICGCGGAGGCGCGGCCAGCTTCCCTTGGATCGGACTTTCCGCCCCTAGGGCCAGGCG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               782 TCCGGGGCTCGGGTGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATTACCCGGGGAAGTG 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                         482 GCACCTCCCCACGCGCGCTCGGCCCCGGGCCACCGCCTTCGTCGGCCCCCCGCCCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  722 CGCGCCAGGCGGACACICCICICGGCTCCCCCGGCAGCGGCGGCGGCGGGGGGGC
                                                                                                                                                      302 GCGGAGCTICAGCCTIGTCCCTTCCCCAGTTTCGGGCGGCCCCCCAGAGCTGAGTAAGCCG
                                                                                                                                                                                                                                                        362 GGTGGAGGGAGTCTGCAAGGATTTCCTGAGCGGGATGGGCAGGAGGAGGGCAAGGGCAA
                                                                                                                                                                                                                                                                                                                                                         422 GAGGGCGCGGAGCAAAGACCCTGAACCTGCCGGGGCCGCGCTCCCGGGCCCGGGTCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; anglogenesis; methylation; eye disease; glaucoma; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human angiogenesis associated polynucleotide SEQ ID NO 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1144 CGAAAAAGGAACTCTAACGAACGTAACCGCG 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  902 CGAGAGGACGCACTCIGGCGGCCGGGTCTTTGGCCGCG 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ67064 standard; DNA; 6321 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-AUG-2002
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                                                                                               Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          their complementary sequences.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the Buropean Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signal transduction associated genes. The DAR sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligomuclectides and/or PAR oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DAR can be obtained from cells or cellular components which contain DAR, e.g. cell lines, blogals, sputum, stool, urine, eerebrial spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The diseases associated with signal transduction e.g. solid tumcers and diseases associated with signal transduction e.g. solid tumcers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genemic sequences of genes associated with signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2044 CCGAAAAAAACACGAACACCCCTAAAACTAAATTCGCAATCTICCCAAAAA 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 TCCGGTGCCTTCCTAGACTTCTCGGGACAGTCTGAAGGGGTCAGGAGCGGCGGGACAGCG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 TGCCAAGCAAGCGTCAGTTCCCCTCAGGCGCTCCAGGTTCAGTGCCTTGTGCCGAGGGTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 CGGGAAGAGCAGGCAAGGGGAACAGCGGCGCTCAGTCCTCCGTGCCAAGAACA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                  Signal transduction associated gene modified complementary DNA #52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to chemically modified DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.8e-93;
0; Mismatches 267; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.3%; Score 510.8; 71.5%; Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 104; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin K;
                                                                                                                                                                                                                                                                                                                                                                            29-JUN-2001; 2001WO-EP07472.
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2000DE-1043826.
  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG
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01-SEP-2000;
23-APR-2002
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1209 ATTAICTCCIARCTARARCGCGARACGCTCARARCGCGARACGACGACGACGACGACGA 1150
    This cLNA clone codes for human soluble FLT-1 (sFLT-1, see AAW44841), the tyrosine ki.ase receptor (TKR) for human vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibition of anglogenesis, particularly in tumours · by using DNA expressing a scluble form of a tyrosine kinase receptor which forms a dimer with a lascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLI-1, SFLI-1; vascular endothelial growth factor; VEGF, sVEGF-RI, receptor tyroside kinase; signal transduction, angiogenesis, gene therapy; tumour; metastasis; inflammation; psoriasis; rheumatoid arthiltis; haemangioma; diabetic retinopathy;
                                                                                                                   1449 PATRABARC COTTARCGICACCARABARARACCGRARIALARARATARACTARAAAA
                                                                                                                                                                 ASSITATAAA SOGCCCCCCCCCCCTCGCTCTTCTTCCATCGAGGTCCGGGGAGGCTCGGAG
                                                                                                                                                                                                                                                          722 CCCCCAGGCHBACACICCICICGGCTOCTCCCGGGCAGCGGCGGGGGGGGCGGAGCGGGC
                                                                                                                                                                                                                                                                                                                                                   782 INCOCAGOTONIGNECAGOGGCCAGCGGCGCCTGGCGGCGAGCATTACCCGGGGAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                          CTIGACGICACCAGAAGGAGGIGCCGGGGIAGGAAGIGGGCTGGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          angiofibroma; mecular degeneration; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human soluble VESF receptor FLT-1 cDNA.
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250..2313
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV19347 standard; DNA; 2313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1998-230425/20.
05: AAW44841.
                                                                     602 GardGaGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-AUG-1998
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AAV19347
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HERKOXEKE
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                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a nucleic acid (I) comprising a segment of 16 bases of chemically prefreated DNA of anglogenesis-associated genes (II) having sequences (ABG6691-ABG67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                          single-nucleotide polymorphisms, in angiogenesis related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, maqular degeneration caused by neovascularisation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2049 CCGAAAAAAACACGGACCCCCCCTAAAACCTAAATTCGCAATCTICCCAAAAA 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1929 TCCGATACCTTCCTAAACTTCTCGAAACAATCTAAAAAATCAAAAACGACGAAACAACG 1870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1629 AAAAACGCGAAACAAAAACCCTAAAACTACCGAAACCGCGCTCCCGAAACCGGGTCGCCA 1573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCAAGCAAGCGTCAGTTCCCCTCAGGCGCTCCAGGTTCAGTGCCTTGTGCCGAGGGTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542 CGTAGCCGCAGGGAAGCGAGCCTGGGAGGAAGAAGAGGGTAGGTGGGGAGGCGGATGAGG 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1989 TACCAAAAGAAAGTCAATTCCCCTCAAAGGCTCCAAATTCAATACCTATATACCGAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 GCACCTCCCCACGCGCGCTCGGCCCCGGGCCACCCGCCTCGTCGGCCCCCGGCCCTTCTC
                                                                                                                                                                                                                             New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 TCCGGTGCCTTCCTAGACTTCTCGGGACAGTCTGAAGGGGTCAGGAGCGGCGGGACAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 CGGGAAGAGCAGGCAAGGGGAGACAGCCGGACIGCGCCICAGICCICCGIGCCAAGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 CCGTCGCGGAGGCGGGCCAGCTTCCCTTGGATCGGACTTTCCGCCCCTAGGGCCAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 GCGGAGCTTCAGCCTTGTCCCTTCCCCAGTTTCGGGGGCCCCCCAGAGCTGAGTAAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 GGTGGAGGGAGTCTGCAAGGATTTCCTGAGCGCGATGGGCAGGAGGAGGGGGCAAGGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.3%; Score 510.8; DB 24; Length 6321; 71.5%; Pred. No. 1.8e-93; Ive 0; Mismatches 267; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6321 BP; 1474 A; 258 C; 1553 G; 3036 T; 0 other;
                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 94; 41pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
06-DEC-2001; 2001WO-EP14320.
                                             2000DE-1061338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 71.5 Matches 671; Conservative
                                                                                           (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                    WPI; 2002-500450/53.
                                             06-DEC-2000;
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                (MERI ) MERCK & CO INC
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P-PSDB; AAW47036.
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                                                                   Kendall RL,
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growth factor (VEGF). PCR cloning was used to obtain the fil-1 derived TRR (sVEGF-RI) sflt-1 cDNA from a HUVEC cDNA library. The invention relates to methods of gene therapy for inhibiting anglogenesis associated with solid tumor growth, tumour metastasis, psoriasis, rheumatoid arthritis, haemangioma, diabetic retinopathy, anglofibroma and macular degeneration. For primary tumour growth and metastasis, this involves tranfer of a nucleotide sequence encoding a soluble form of VEGF TRR to a mammalian (human) host, preferably using an adenovirus or recombinant plasmid DNA vector. The transferred nucleotide sequence transcribes mink and a soluble receptor protein which binds to VEGF in extracellular regions adjacent to the primary tumor and vascular endothelial cells. Formation of a sVEGF PLYRGF comptex prevents binding of VEGF-Rabe the signals associated with vascular endothelial cell-induced tumour anglogenesis. Expression of a soluble TRR may also impart a signals associated with vascular endothelial cell-induced tumour anglogenesis. Expression of a soluble TRR may also impart a therapeutic effect by binding either with or without VEGFs to form thereby inhibiting the mitogenic and anglogenic activities of the present the present anglogenic activities of sequence and sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   730 GOGGACACTCCTCTCGGCTCCTCCCGGCAGCGGCGGCTCGGAGCGGGCTCCGGGGC 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19; Length 2313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 154.8; DB 15; Length
Pred. No. 3.2e-30;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor/inhibitor (SVEGF-RI) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2313 BP; 705 A; 537 C; 539 G; 532 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= " soluble VEGF inhibitor'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           910 CGGACTCTGGCGGCCGGGTCTTTGGCCGCGGG 941
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250..2313
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98.1%;
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93US-0038769.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 98.1 Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
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AAV09330
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                                                                                                                                                                                                                                                                                                     fragment of the VEGF receptor that binds VEGF with high affinity but is unable to transduce a signal. sVEGF-RI is used to inhibit VEGF activity, specifically VEGF-Induced angiogenesis, particularly for treatment of pscriasis, rheumatoid arthritis, haemanglomas, angiofibromas, diabetic retinopathy, neovascular glaucoma or tumour vascularisation. The sVEGF-RI can be administered topically or intravenously or from slow-release
                                                                                                                                                                                                                                                    growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEGF; human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 730 GCGGACACICCICTCGGCTCCTCCCCGGCAGCGGCGCGCTCGGAGCGGCTCCGGGGC 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amplification; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product- "VEGF receptor extracellular domain" /note= "no stop codon is given at the 3' end of the
                                                                                                                                                                                                                                              cDNA encodes a soluble inhibitor of vascular endothelial cell
or (VEGF). The VEGF receptor/inhibitor (SVEGF-RI) represents a
                         growth factor receptor - and related vector and transformed cells, expressing scluble inhibitor of VEGF useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           790 TCGGGTGCAGCGGCCAGCGGCCCTGGCGGCGAGGATTACCCGGGGAAGTGGTTGTCTC
                                                                                          angiogenesis: e.g. for treatment of psoriasis, arthritis, tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19; Length 2313;
Nucleic acid encoding soluble form of vascular endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human VEGF receptor extracellular domain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2313 BP; 705 A; 537 C; 539 G; 532 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin-like domain; extracellular domain; vascular endcthelial cell growth factor receptor; truncation; mutant; tumour; vascularisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 194.8; DB 1997 Pred. No. 3.2e-30;
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                                                                                                                                                                                 Claim 3; Fig 2A-B; 47pp; English.
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iiarity 98.1%;
Conservative 0
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This is the nucleotide sequence encoding the lst-7th immunoglobulin-like domains of the extracellular domain of VEDF (vascular endothelial cell growth factor) receptor FLT. The sequence is amplified by the primars ANV01458-V01459. The VDGF receptor sequence can be used to generate truncated mutants which comprise the immunoglobulin-like domains 1-3, 1-4, 1-5 or 1-7. The polypeptides can be used in treatment of solid tumours and other diseases accompanied by pathological vascularisation since they inhibit vascularisation by stimulation with VEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        850 CIGGUIGGAGUCGCGAGACGGGCGTCAGGGCGCGGGGCCGGCGGCGGCGAACGAGGA 909
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                                                                                                                                                                                                                                                               Vascular endothelial growth factor binding polypeptide(s) - used in the treatment of solid tumours etc.
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Pred. No. 3.2e-30;
0; Mismatches 2; Indels 2;
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                                                                                                                                                                                                                                                                                                             Disclosure; Page 9-12; 19pp; Japanese.
                                                                                                                                                                          (TOAG ) TOA GOSEI CHEM IND LTD.
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Best Local Similarity 98.1%;
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
a 255 c 1549 g 3038 t
                                                                                                                                                              782 ICCGGGGCTCGGGTGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATTACCCGGGGAAGTG 841
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                                                       AGGITATAAATCGCCCCCCCCCCCCCCCCCCCCCCCCCGGAGGCCCCGGAGGCTCCGAG
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Diagnosis of diseases associated with the cell cycle
Patent: WO 0168911-A 130 20-SEP-2001;
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AXX51869.1 GI:15985224
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1 (bases 1 to 6316)
OleK.A., Piepenbrock.C. and Berlin.K.
Diagnosis of diseases associated with tumor suppressor genes and oncogenes.
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/note="chemically treated genomic DNA (Homc sapiens)"
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71.5%; Pred. No. 6.8e-74;
Live 0; Mismatches. 267; Indels
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5172 ACGAGGACGGATTITGGCGGTCGGGTCGTTGGTCGCGGG 5212
                                                                                                                                    DNA
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Epigenomics AG (DE)
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Sequence 74 from Patent WO0168912.
AX251106
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 TGCCAAGCAAGCGICAGIICCCCICAGGCICCAGGIICAGIGCCIIGIGCGAGGGIC 121
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                                                    TCCGGTGCCTTCCTAGACTTCTCGGGACAGTCTGAAGGGGTCAGGAGCGGGGGACAGCG
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Diagnosis of diseases associated with cell signalling Patent: WO 0202807-A 106 10-JAN-2002; Epigenomics AG (DE)
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Pred. No. 6.8e-74;
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/note="chemically treated genomic DNA (Homo sapiens)"
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Pred. No. 6.8e-74;
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AX458548
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                                                                                                                                                                                                                                                                                                                                                            Contact: hgsc.help@bcm.tmc.edu
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Center clone name: CH230-448N2
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                                                                                                                                                                                                                                                                                   COMMENT
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Rattus norvegicus clone CH230-448N2, *** SEQUENCING IN PROGRESS
***, 57 unordered pieces
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                1269 TCCGAAACTCGAAIACAACGACCAACGAACGCCIAACGACGAAAAIIACCCGAAAAAIA 1210
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 57 conligs. The true order of the pieces is not known and their order in this sequence record is
Sutton.A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vagquez,L., Vara,V., Villalon,D., Vison,R., Wang,A., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallinams,G., Williams,G., Wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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123336: gap of unknown length
127745: contig of 4209 bp in length
137745: gap of unknown length
133361: contig of 5716 bp in length
133451: gap of unknown length
140523: contig of 7062 bp in length
14090: contig of 7062 bp in length
14090: contig of 3467 bp in length
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Search completed: December 8, 2002, 11:46:32 Job time: 2551.64 secs AL547815

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AU136034 AU36034 PLACEL Homo sapiens cDNA clone PLACE1003403 5', mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 697)
Ota. T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute: CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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Genomics Laboratory
Helix Research Institute
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Site_2: EcoRV (destroyed); RNA source anonymous pool of
male brains, age range 23-27 yo. Library is oligo-dī
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
Day Sequencing by: Incyte Senomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/clone_lib=PLACE1"
/tissue_type="placenta"
/note="Vector: pME188FL3"
a 185 c 220 g 126 t
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                                  /organism="Homo sapiens"/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Location/Qualifiers
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BIB20974 906 bp mRNA linear EST 04-OCT-2001 603035625F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176591 5'.
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/note="Organ: pooled brain, lung, testis; Vector:
pcMv-SPORIG, Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; I
male lung, age 27; and 1 male testis, age 69. Library is
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                                                                                                                            Note:
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primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 Kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Not take is a NIH.MGC Library."
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostori;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Plate: LLAM11440 row: a column: 08
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Pred. No. 5.9e-35;
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/db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.
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High quality sequence stop: 765.
Location/Qualifiers
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/note="Vector: pCMV-SPORT6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
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AL541018
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4503748
This clone has the following problem: incomplete processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIC 20-MAY-2002
                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1171)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission Submitted (C6-MAY-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Collection (MGC), Cancer Genomics Office, National Cancer.
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing Center
Center code: BCM-HGSC
Vebsite: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaxatae, P. H., Garcia, A.M., Lu, X., Huljk, S.W., Hale, S.W.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Marrin, R.G., Muzny, D.M.
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
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      code
                                                                                                                                                                                       887
                                                                                                                                                                                                                                                                                                              61 GCTCGGAGCGGCTCCGGGGCTCGGGTGCAGCGGCCAGCGGGCGCCTGGCGGGGGAGGAT 120
                                                                                                                                                                                                                                                                      768 GGCTCGGAGCGGGCTCCGGGGCTCGGGTGCAGCGGCCAGCGGGCGCCTGGCCGCGGAGGAI 827
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                               1 CGGGAGGCICGGAGCGCCCAGGCGGACACICCICTCGGCICCICCCCGGCAGCGGCGGC
                                                                                                                                                                                                                                                                                                                                                     828 TACCCGGGGAAGIGGIIGICICCIGGCIGGAGCCGCGAGACGGGCGCICAGGGCGCGGGG
                                                                                                                                                                                                                                                                                                                                                                         121 TACCCGGGAAGIGGIIGITGICCCGGCGGAGACCGGGGGCGCCCAGGGGGGG
Gruber (Invitrogen). Research Genetics tracking 021. Note: this is a NIH_MGC Library."

228 c 264 g 194 t l Others
                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                         Score 230.8; DB 13; Length 906;
                                                                                                                        Pred. No. 1.2e-34;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1171 bp mRNA
Homo sapiens, clone IMAGE:5175591, mRNA.
BC029849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                                                      Query Match 24.5%;
Best Local Similarity 99.1%;
Matches 232; Conservative
          021: NU.
228 C
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                                       219 a
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                                       BASE COUNT
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VERSION
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BC029849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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SOURCE

COMMENT

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cDNA was primed with a Noti-oilgo(dT) primer. Five prime and enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMySPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville (Maryland 2080, USA Fax : (1) 301 610 8371 Email : fliangelifetch.com URL : http://fulllength.livviltogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL541018 LII_FL002_PL1 Homo sapiens cDNA clone CSODE005Y102 5 prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 826)
II,W. B., Gruber.C., Jessee,J. and Polayes,D.
FUI:-Ingfth CDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
                                                                                                                                                                                                                                                                                  887
                                                                                                                                                                                                                                                                                                                                                                                            121 TACCCGGGGAAGIGGIIGICTCCCGGCGGGACGCGCGAGACGGGCGCTCAGGGCGCGGGGG 180
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                                                                                                                                                                                                                                                   758 GGCICGEAGCGGGCTCCGGGGCTCGGGTGCAGCGGCCGGCGCCTGGCCGGCGAGGAI 827
                                                                                                                                                                    1 CGGGAGGCTCGGAGCGCGCCAGGGGGACACTCCTCTCCGCTCCTCCCCGGCAGCGGCGCC 60
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                                                                                     Gaps
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BP 191 91005 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                 828 TACCCGGGGAAGTGGTTGTCTCCTGGCTGGAGCCGCGAGACGGGCGCTCAGGGCGCGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CCGCCGCCGCGAACGAAGAGGACGGACTCTGGCGGTCGGCGGTGGCCGCGGG 234
                     DB 11; Length 1171;
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Score 230.8; DB 11; Deuy...
Pred. No. 1.2e-34;
...--rohes 2; Indels
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/lab_host="DH10B"
                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                     24.58;
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Matches 225; Conservative
                                                                            Matches 232; Conservative
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Appli Appli Appli Appli

Sequence 5 Sequence 1 Sequence 1 Sequence 1 Sequence 2 Sequence 2

US-08-446-648-45 PCT-US95-0428-45 US-08-22-538-5 US-09-427-353-1 US-08-78-141A-5 US-08-78-141A-5 US-08-222-616-17 PCT-US95-0428-17 US-08-306-691B-21

Sequence 45, A Sequence 45, A Sequence 5, Ap Sequence 1, Ap

3, Appli 3, Appli

Sequence Sequence

PCT-US93-06251-25

US-08-222-299-3 US-08-434-878-3 Sequence

Sequence 1, Sequence 1,

US-08-183-211-1 PCT-US95-00176A-1 PCT-US95-03718-3

ALIGNMENTS

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2313
2651
551
6827
6827
5084
5084
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               US-09-098-707A-1
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               541.6
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                                                                (without alignments) 7710.006 Million cell updates/sec
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                                                      December 8, 2002, 09:24:02 ; Search time 83.5704 Seconds
                                                                                       X51602_COPY_1900_4000
2101
1 TATATCACAGAIGIGCCAAA.......CGACAGCAGCACTCIGIIGG 2101
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                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCUGCOMB.seq:*
     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-930-548A-7
US-08-443-861-1
US-08-43-861-1
US-07-913-8298-1
US-07-97-451-5-
US-07-96-507-3
US-08-252-517-5
US-08-601-891-5
US-09-601-891-5
                                                                                                                                                                tal number of hits satisfying chosen parameters:
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PCT-US92-08401-5
PCT-US92-0893-5
US-08-232-538-17
US-08-786-164-17
US-08-340-011-1
US-08-340-011-1
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                                                                                                                                                   441362 seqs, 153338381 residues
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                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                      nucleic search, using sw model
                                                                                                                         Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. 8.5e-212;
0; Mismatches 562; Indels 6;
                                                                                                                                    Tebben, Andrew J.
TILLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
VIVHER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 07065-0807
ZOMPLIER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IPM PC POSyMS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/ACENT INFORMATION:
NAME: Hand, J. Marx
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19963PV
TELECOMUNICATION INCOMATION:
TELEPHONE: 722/54-305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,707A
FILING DATE: 17-Jun-1998
CLASSIFICATION: <U0Known>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                               ADDRESSEE: Merck & Co., Inc. STREET: P.O. Box 2000
Sequence 1, Application US/09098707A
Patent No. $204011
GENERAL INFORMATION:
                                                                                                 Thomas, Kenneth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4071 base pairs
IYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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Matches 1077; Conservative
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Sequence

PCI-US95-04228-31

Sequence

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GALTATACTACACCAGAAAIGTACCAGACCAIGACTGCTGCTGCAGCGGGGGGGCCCA 3442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGAGACCCAGGIIIICAGAGIIGGIGGAACAIIIGGGAAAICICIIGCAAGCIAAIG 3502
                   JIGCCCGGGAIAITIATAAGAACCCCGATTATGTGAGAAAAGGAGATACTCGACTTC 1534
                                                                                                                                                                                                                                            GASTACTCTACTCCTGAAATCTATCAGATCATGCTGGACTGCTGGCACAGAGACCCAA 1774
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ASTITICAAGIGGCCAGAGGCAIGGAGTICCIGTCITCCAGAAAGIGCAITCAICAGG 1414
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                                                                                                                                                                                                                       CIGNAATGGATGCCTCCCGAATCTATCTTTGACAAATCTACAGCACCAAGAGCGACG 1594
                                                                                                                                                                                                                                                                                                  ISSICTIACSSAGIALISCIGIGGGAAATCTICICCITAGGIGGGICICCATACCCAG 1654
                                                                                                                                                                                                                                                                                                                                                                         STACAAATGGATGAGGACTTTTGCAGTGGCCTGAGGGAAGGCATGAGGATGAGAGCTC 1714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANT: Kendall, Richard L.
ANT: Thomas, Kenneth A.
ANT: Thomas, Kenneth A.
ANT: Tebben, Andrew J.
PE INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
PENDENCE: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIPE: Floppy disk
TER: Floppy disk
TER: EBW PC compatible
TING SYSIEM: PC-DOS/MS-DOS
ARE: Patentin Release #1.0, Version #1.30
APPLICATION DAIA:
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E: Hand, J. Mark
ESTRATION NUMBER: 36,545
ERENCE/DOCKET NUMBER: 19963PV
OMUNICATION INFORMATION:
EPHONE: 732/594.3905
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). Box 2000
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07055-0907
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                                                                                                           Length 4071;
                                                                                                           Score 713.8; DB 4;
Pred. No. 8.5e-212;
0; Mismatches 562;
                                                                                                                                     0;
                                                                                                            Query Match
34.0%;
Best Local Similarity 65.5%;
Matches 1077; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 4071 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                     MOLECULE IYPE: CDNA
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                                                     TOPOLOGY:
                                                                                 US-09-483-539-1
                                                                                                            Query Match
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2786 GGAGCAACAGAAATGAATTTGTCCCCTACAAGACCAAAGGGGGCACGATTCCGTCAAGGG 2845
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                                                                                                                                            2846 AAGACTACGTTGGAGCAATCCCTG----TGGATCTGAAACGGCGCTTGGACAGCATCACCA
                                                                                                                                                                                                       GCAGCGAAAGCTTTGCGAGCTCCGGCTTTCAGGAAGATAAAAGTCTGAGTGATGTTGAGG
                                                                                     AAGAAAAATGGAGCCAGGCCTGGAACAAGGCAAGAAACCAAGACTAGATAGCGTCACCA
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ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
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Patent No. 576660
GENERAL INFORMATION:
APPLICANT: Terman, Bruce I.
APPLICANT: Carrion, Miguel E.
7111E OF INVENTION: Tention factorion
7111E OF INVENTION: Pactor Receptor
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COMPUTER: IBM PC compatible
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COMPUTER READABLE FORM:
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US-07-930-548A-7
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRELICATION NUMBER: US/08/810,116
FILING DATE: 25-FEB-1997
                                                                                                                                                                                                                                                                                                                                                               Query Match 33.8%; Score 710.6; DB 1; Best Local Similarity 65.3%; Pred. No. 8.5e-211; Matches 1075; Conservative 0; Mismatches 564;
                                                                                                                                                31,298-01
                                                               PRIOR APPLICATION DAIA:
APPLICATION NUMBER: 07/930,548
FILING DAIE: 23-NOV-1992
ATTORNEY/AGENI INFORMATION:
                                                                                                                                  30,637
                                                                                                                                            REFERENCE/DOCKET NIMBER: 31
IELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                            LENGTH: 4236 base pairs
                                                                                                                                                                               IELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                      NAME: Gordon, Alan M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                          nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                     linear
                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                           NAME/KEY:
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US-08-810-116-7
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                                                                                                                                                                                                                                                         2963 AACAGGAAGCTCCTGAAGATCTGTATAAGGACTTCCTGACCTTGGAGCATCTCATCTGTT 3022
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                                                                                                                                                         TGTTGAAAGAAGAAGAACAACACAGGGATCGAGCTCTCATGTCTGAACTCAAGATCC 2665
                                                                                                                                                                                                                                                                                                                                          GAGGGCCICTGATGGTGATTGTTGAATACTGCAAATATGGAAATCTCTCCAACTACCTCA 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAGCAAACGIGACITAIITITCICAACAAGGAIGCAGCACIACAACAIGGAGCCIAAGA 1174
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                                                                                                            IGCIGAAAGAGGGGGCCACGGCCAGGGAGTACAAAGCTCTGATGACTGAGCTAAAAATCT 994
                                                                                                                                                                                                                        GAGGGCCACTCATGGTGATTGTGGAATTCTGCAAATTTGGAAAACCTGTCCACTTACCTGA
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                                                ITGAAGCAGATGCCITTGGAATTGACAAGACAGCAACTTGCAGGACAGTAGCAGTCAAAA
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2666 TCATICATAITGGTCACCATCICAATGTGGTCAACCTTCTAGGTGCCTGTACCAAGCCAG 2725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2606 IGTIGAAAGAAGAACAACAACAGIGAGCATCGAGCICTCATGIGAGATCC 2665
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             2246 AGGCATITITCAIAATAGAAGGTGCCCAGGAAAAGACGAACTTGGAAATCATTAITCING 2305
                                                                                       2486 TCCCCAGAGAGCGGCTGAACCTAGGTAAGCCTCTTGGCCGTGGTGCCTTTGGCCAAGAGA 2545
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                                                                                                                                                                                                                                                             755 AIGAAGTICCITIGGAIGAGCAGTGIGAGCGGCTCCCTTAIGAIGCCAGCAAGIGGGAGI 814
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                                                          638 CAIGCACCIGIGIGGCIGCGACTCITICIGGCICCIATTAACCCICCIIAICCGAAAAA 597
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Sequence 7, Application US/07930548A
Patent No. 5861301
GENERAL INFORMATION: Bruce I.
APPLICANT: Cartion, Miguel E.
TITLE OF INVENTION: Identification of a No. 5861301e1 Human Growth
TITLE OF INVENTION: 12 actor Receptor
NUMBER OF SEQUENCES: 12
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Pred. No. 8.6e-211;
0; Mismatches 564; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/930,548A FILING DATE: 23-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31,298-01
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSIEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKEI NUMBER: 31
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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ilarity 65.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                               STATE: New Jersey COUNTRY: U.S.A. ZIP: 07470
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1715 CTGAGTACTCTACTCCTGAAATCTATCAGGATCATGCTGGAGCTGGTGGCAGCAGAGACCCAA 1774
                  1775 AAGAAAGGCCAAGAIIIGCAGAACIIGIGGAAAAACIAGGIGAIIIGCIICAAGCAAAIG 1534
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                                                                                        3443 GICAGAGACCCAGGIIICAGAGIIGGIGGAAAATCICIIGGAAAGCIAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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65.0%; Pred. No. 1.6e-210;
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ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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APPLICATION WUMBER: US 08/193,829
FILING DATE: 09-FEB-1994
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 7683-060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/443,861
FILING DATE: 22-MAY-1995
                                                                                                                                                                            3503 CICAGCAGGAIGGCAAAGACIACAI 3527
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5851999
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TELEPHONE: (212)790-9090
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APPLICANT: Millauer, Birgit
APPLICANT: Gazit, Ayiv
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACIERISTICS:
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Best Local Similarity
Matches 1081; Conserva
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RY: U.S.A.
10036-2711
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US-08-443-861-1
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                                                           ISCICAAGATAAGAACAACAAAAAAAAATIGCCIGGICAAAAAACACICAICAICAICCIAGA 2267
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CAACCACAAAATACAACAAGAGCCIGGAAITATTITAGGACCAGGAAGCAGCACGTGIT 500
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1338 GGAAGAICIGAITICIIACAGITTICAAGIGGCCAGAGGCAIGGAGIICCIGICIICCAG 1397
                                                                                                                                                        3405 IAAGAICTGIGACIICGGCIIGGCCCGGGACAIIIAIAAAGACCCCGCAIIAIGICAGAAA 3454
                                                                                 1578 CAGCACCAAGAGCGACGIGIGGICTIACGGAGTATIGCTGIGGGAAATCTICTCCTTAGG
                                                             1398 AAAGIGCAITCAICGGGACCIGGCAGCGAGAACAIICITIIAICIGAGAACAACGIGGI
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APPLICANT: Gazit, Aviv
APPLICANT: Levitzki, Aviv
IIILE OF INVENTION: FIk-1 Is A Receptor For Vascular
IIILE OF INVENTION: Endothelial Growth Factor
MOMBER OF SEQUENCES: 6
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CURRENI APPLICATION DATA:
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STREET: 1155 Avenue of the Americas
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09-FEB-1994
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COMPUTER: IBM PC compatible
OPERATING SYSIEM: PC-DOS/MS-DOS
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; Patent No. 6177401
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IELECOMMUNICATION INFORMATION:
IELEPHONE: (212)790-9090
IELEFAX: (212)869-9741
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APPLICANT: Ullrich, Axel
APPLICANT: Risau, Werner
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ADDRESSEE: Pennie &
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COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
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FILING DATE: 09-FEB
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                                                                                                                                                                                                                                                                                                                        33.8%; Score 710; DB 4; Length 54 65.0%; Pred. No. 1.6e-210; Live 0; Mismatches 575; Indels
IELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACIERISTICS:
LENGTH: 5470 base pairs
TYPE: nucleic acid
SIRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 65.0
Matches 1081; Conservative
                                                                                                                                                                                                                       CDS
285..4385
                                                                                                                                                unknown
                                                                                                                                                TOPOLOGY: un
                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                           US-08-193-829B-1
                                                                                                                                                                                                  FEATURE:
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COMPUTER READABLE FULL.
MEDIUM IYPE: Floppy disk
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PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-40N-1991
FRICR DATE: 28-40N-1991
FRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
                                    COMPUTER: IBM PC compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/07/813,593
FILLING DAIE: 19920415
CLASSIFICATION: 435
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SEQUENCE CHARACTERISTICS:
LENGTH: 5406 base pairs
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                              2988 CGCCTGCACCAAGCCGGAGGGCCTCTCATGGTGATTGTGGAATTCTGCAAGTTTGGAAA 3047
                                                                                        1158 ACACATGGAGCCTAAGAAAAAAATGGAGCCAGGCCTGGAACAAGGCAAGAACCAAG 1217
                                                                                                                                                       3108 ACCTICCGCCAGGCCAAGGACTACGTIGGG---GAGCICICCGTGGAICIGAAAAGACG 3164
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LEM-3-PPP

REFERENCE/DOCKET NUMBER: LE

: 212-645-1405 212-645-2054

TELEPHOME:

5406 base pairs

NUCLEIC ACID

SIRANDEDNESS:

28,601

FILING DATE: 02-APR-1991 ALIORNEY/AGENT INFORMATION:

NAME: Feit, Irving N. REGISTRATION NUMBER:

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2190 GCSCAIGGCACCAIGAICACCGGAAAICIGGAGAAICAGGACAAIGGGGGAGAC 2249
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                                                     Indels
33.7%; Score 708.4; DB 1; 65.0%; Pred. No. 4.9e-210;
                                                     0; Mismatches 576;
                                                     Conservative
                         Local Similarity
                                                     Matches 1080;
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GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
IIILE OF INVENTICN: TOIDFOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTICN: RECEPTORS AND THEIR LIGANDS

Sequence 3, Application US/07813593 Patent No. 5185438

-07-813-593-3

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSIEMS INCORPORATED
STREET: 180 VARICK STREET

CIIY: NEW YORK STAIE: NEW YORK COUNTRY: U.S.A. STATE: NEW COUNTRY: U.S

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Length 5406;

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NAME/KEY: LOCATION:

FEATURE:

LOCATION: 208..4311

NAME/KEY:

MOLECULE IYPE: CDNA

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PRIOR APPLICATION DAIA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DAIE: 26-JUN-7
PRIOR APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
FILING DATE: 02-APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                           New York
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
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2490 GGAAGICAITAITCITGITGGGGGACTGCAGGATIGCCAATGITCITGITGGCTCCTTCITGIT 2549
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                                                            1458 GAAGAIIIGIGAIIIIIGGCCIIGCCCGGGAIAIIIAIAAGAACCCCGAIIAIGIGAGAAA 1517
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IIILE OF INVENTION: ICLIPOTENT HEMATOPOLETIC STEM-
IIILE OF INVENTION: RECEPTORS AND THEIR LIGANDS
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OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19921119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ImClone Systems Incorporated SIREET: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DAIE: 25-UNN-1992
PRIOR APPLICATION DAIA: APPLICATION NUMBER: US PCI/US92/05401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: TW 81102961
FILING DAIE: 15-APR-1992
PRIOR APPLICATION DAIA:
APPLICATION NUMBER: US PCI/US92/02750
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
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28-JUN-1991
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02-APR-1991
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APPLICATION NUMBER: US UNASSIGNED
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FILING DAIE: 26-JUN-1992
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US-07-977-451-5
: Sequence 5. Application US/07977451
: Patent No. S270458
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SEQUENCE CHARACTERISTICS:
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Pred. No. 4.9e-210;
0; Mismatches 575;
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Best Local Similarity 65.0%;
Matches 1080; Conservative
                                                      ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                       sig_peptide
208..264
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265..4308
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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208..4311
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IIILE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM IIILE OF INVENTION: RECEPTORS AND THEIR LIGANDS NUMBER OF SEQUENCES: 4
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ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
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Patent No. 5283354
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2250 CATIGAAGIGACIIGCCCAGCAICIGGAAAICCIACCACCACAIIRCAIGGIICAAAGA 2309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 ICAGGAAGCACATACCTCCTGCGAAACCTCAGTGATCACACAGTGGCCATCAGCAGTIC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 CAACCACAAAATACAACAAGAGCCTGGAATTATTTTAGGACCAGGAAGCAGCACGCTGTT 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.7%; Score 708.4; DB 1; Length 5405; 65.0%; Pred. No. 4.9e-210; tive 0; Mismatches 576; Indels 6;
                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatchtLn Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,507
                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/813,593.
FILING DATE: 24-DEC-1991.
PRIOR APPLICATION NUMBER: US/07/793,065.
FILING DATE: 15-NOV-1991.
PRIOR APPLICATION NUMBER: US/07/728,913.
FILING DATE: 28-JUN-1991.
PRIOR APPLICATION NUMBER: US/07/728,913.
FILING DATE: 28-JUN-1991.
PRIOR APPLICATION NUMBER: US/07/579,665.
FILING DATE: 02-APR-1991.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEM-3-PPP
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LES
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
                                                                                         : Floppy disk
IBM PC compatible
STREET: 180 VARICK STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5406 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   FILING DATE: 19920917
CLASSIFICATION: 535
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208..4308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                          COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208..4311
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Best Local Similarity
Matches 1080; Conserv
                                NEW YORK
                                               U.S.A.
                CITY: NEW YORK
                                                            10014
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US-07-946-507-3
                                                                                                           COMPUTER:
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                                               COUNTRY:
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1398 AAAGIGCATICATGGGGACCIGGCAGGGAAACATCTTTTATCTGAGAACAACGIGGT 1457
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                                                                                                                       621 GGAGCIGALCACICIAACAIGCACCIGIGIGGGCIGCGACICITICIGGCICCIAITAAC 680
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561 GGCCTCTGTGGAAAGTTCAGCATACCTCACTGTTCAAGGAACCTCGGACAAGTCTAATCT
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2070 CAICTTÉAILGIGGCATTICAGAATGCCTCTCTGCAGGACCAAGGCGACTATGTTIGCTC 2129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.7%; Score 708.4; DB 1;
65.0%; Pred. No. 4.9e-210;
tive 0; Mismatches 576;
    REGISTRATION NUMBER: 28,601 REFERENCE/DOCKET NUMBER: LEITELECOMMUNICATION INFORMATION:
                                                                                                               INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACIERISTICS:
LENGIH: 5406 base pairs
                                                                  TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
                                                                                                                                                                                                                                                                                                                      N-terminal
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Best Local Similarity 65.0%
Matches 1080; Conservative
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208..254
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265..4308
                                                                                                                                                                                 nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                              CDS
208.4311
                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                linear
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2
                                                                                                                                                                                                      SIPANDEDNESS:
                                                                                                                                                                                                                                                                                                                      FRAGMENI TYPE:
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LOCATION:
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LOCATION:
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: LOCATION:
US-08-252-517-5
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3447 CACAATICAGAGGGAIGIGIGGICITICGGIGIGIIGCICIGGGAAAIAIIIICCIIAGG 3506
                                          1638 IGGGTCTCCATACCCAGGAGTACAAATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGG 1697
                                                                    1698 CATGAGGATGAGAGCTCCTGAGIACICIACTCCTGAAATCTAICAGAICATGCTGGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTROCIENT HEMATOPOIETIC STEM CELL.
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
TOTROF OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                         1818 ITIGCITCAAGCAAHGTACAACAGGAHGGHAAAGACHAGAF 1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 31-OCI-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Inclone Systems Incorporated
SIREET: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DAIA:
APPLICATION WABER: US PCI/US92/02750
FILING DAIF: 02-AFP-1992
PRIOR APPLICATION DAIA:
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15-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 07/728,913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/977,451 FILING DATE: 19-NOV-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08252517 Patent No. 5548055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 15-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 25-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81
FILING DATE: 15-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUN-1991
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MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
FILING DATE: 28-JUN-1
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FILING DATE: 15-NOV
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858 GGCITIIGGAAAAGIGGIICAAGCAICAGCAIIIGGCAIIAAGAAAICACCIACGIGCCG 917
                                          978 GACIGAGCIAAAAAICIIGACCCACAIIGGCCACCAICIGAACGIGGIIAACCIGGIGGG
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                                                            STEM CELL
                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSIEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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Pred. No. 4.9e-210;
0; Mismatches 576;
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
IILLE OF INVENTION: IOIIPOIENI HEMATOPOIETIC STITILE DE INVENTION: IOIIPOIENI HEMATOPOIETIC STITILE DE INVENTION: RECEPTORS AND THEIR LIGANDS NUMBER OF SEQUENCES: 6
                                                                                                                                          INCORPORATED
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APPLICATION NUMBER: US/07/906,397A
FILING DATE: 19920626
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APPLICATION NUMBER: US 07/679,666
FILING DATE: U2-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/813,593 FILING DATE: 24-DEC-1991 PRICR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
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FILING DATE: 28.JUN-1991
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REFERENCE/DOCKET NUMBER: LE
TELECOMMUNICATION INFORMATION:
IELEPHONE: 212-645-1405
                                                                                                               CORPESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS
SIREET: 180 VARICK SIREET
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65.0%;
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  Floppy disk
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IYPE: NUCLEIC ACID
STRANDEDNESS: single
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Bost Local Similarity 65.0
Matches 1080; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                  NEW YORK
: U.S.A.
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CLASSIFICATION:
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CITY: NEW
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RESULT 11 US-07-906-397A-5 : Sequence 5, Application US/07906397A

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                         1518 AGGAGATACICGACTICCICIGAAAIGGAIGGCICCCGAAICTAICTIIGACAAAAICIA 1577
                                                                                                                                                            1578 CASCACCAAGAGGACGIGIGGICITACGGAGIAIIGCIGIGGGAAAICIICICCIIAGG 1637
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IIILE OF INVENTION: TOTIPOTENT HEMATOPOLETIC STEM CELL
IIILE OF INVENTION: RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1818 IIIGCTICAAGCAAAIGTACAACAGGAIGGIAAAGACTACAT 1859
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MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENI APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: ImClone Systems Incorporated
180 Varick Street
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APPLICATION NUMBER: US 07/977,451
FILING DATE: 19-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US 07/906,397
26-JUN-1992
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15-APR-1992
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US-08-601-891-5
; sequence 5, Application US/08601891
; Patent No. 5547651
; GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
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65.0%; Pred. No. 4.9e-210;
tive 0; Mismatches 576;
                                  APPLICATION NOMBER: US 0//93,055
FILING DATE: 15-NOY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0//728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION NUMBER: US 0//579,666
FILING DAIE: 02-AFP-1991
ATTORNEY/AGENT INVERSET US 0//579,666
FILING DAIE: US 0//5
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 5406 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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2550 carreregacegacegradesegecaargaageggaacrgaagacagecraerrere 2609
                                                                                                                                                                                                             TCTCTCCCAACTACCTCAAGAGCAAAGGTGACTTATTTTTTTCTCAACAAGGATGCAGCACT 1157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.7%; Score 708.4; DB 2; Best Local Similarity 65.0%; Pred. No. 4.9e-210; Matches 10809; Conservative 0; Mismatches 576;
                                                                                                              N-terminal
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   MOLECULE IYPE:
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LOCATION:
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US-09-021-324-5
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                                                                                                       1818 TITGCITCAAGCAAATGIACAACAGGAIGGIAAAGACTACAI 1859
                                                                                                                                           3687 CCICCIGCAAGCAAAIGCGCAGGAIGGCAAAGACIAIAI 11
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APPLICATION NUMBER: US/09/021,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Imclone Systems Incorporated STREET: 180 Varick Street
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PRIOR APPLICATION DAIA:
APPLICATION NUMBER: US 07/728 017
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APPLICATION NUMBER: US/07/977,451
FILING DAIE: 1992-11-19
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PRIOR APPLICATION DAIA:
APPLICATION WUMBER: US 07/906,397
FILING DAIE: 26-JUN-1992
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PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
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02-APR-1991
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COMPUTER: IBM PC compatible
OPERATING SYSIEM: PC-DOS/MS-DOS
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Patent No. 5912133
Patent No. FORMATION
APPLICANT: Lemischka, Ihor R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-JUN-1992 PRIOR APPLICATION DATA:
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AITORNEY/AGENI INFORMATION:
NAME: Feit, Irving N.
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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TELEFAX: 212-645-2054
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PRIOR APPLICATION DAIA:
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COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy of
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
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US-09-021-324-5
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2490 GGAAGICAITAICCICGICGGCACIGCAGIGAITGCCAIGTICTICTGGCTCCTICTGT 2549
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             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERRAITING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 708.4; DB 5;
Pred. No. 4.9e-210;
0; Mismatches 576;
                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US92/02750
FILING DATE: 19920402
                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: FEIT, IRVING N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-
IELECOMMONICATION INFORMATION:
IELEPHONE: 212-645-1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.78;
65.08;
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACIERISTICS:
LENGIH: 5405 base pairs
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Best Local Similarity 65.0 Matches 1080; Conservative
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208..4311
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STRANDEDNESS: singl
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LOCATION:
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NAME/KEY:
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FCI-US92-02750-7
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2850 GICIGAACICAAGAICCICAICCACAIIGGICACCAICICAAIGIGGIGAACCICCIAGG 2909
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                                       1038 AGCCIGCACCAAGGAAGAGGGCCICIGAIGGIGAIIGIIGAAIACIGCAAAIAIGGAAA
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TILLE OF INVENTION: Receptors and Their Ligands
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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GENERAL INFORMATION:
APPLICANT: LEMISCHKA, IHOR R.
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PCT-US92-02750-7
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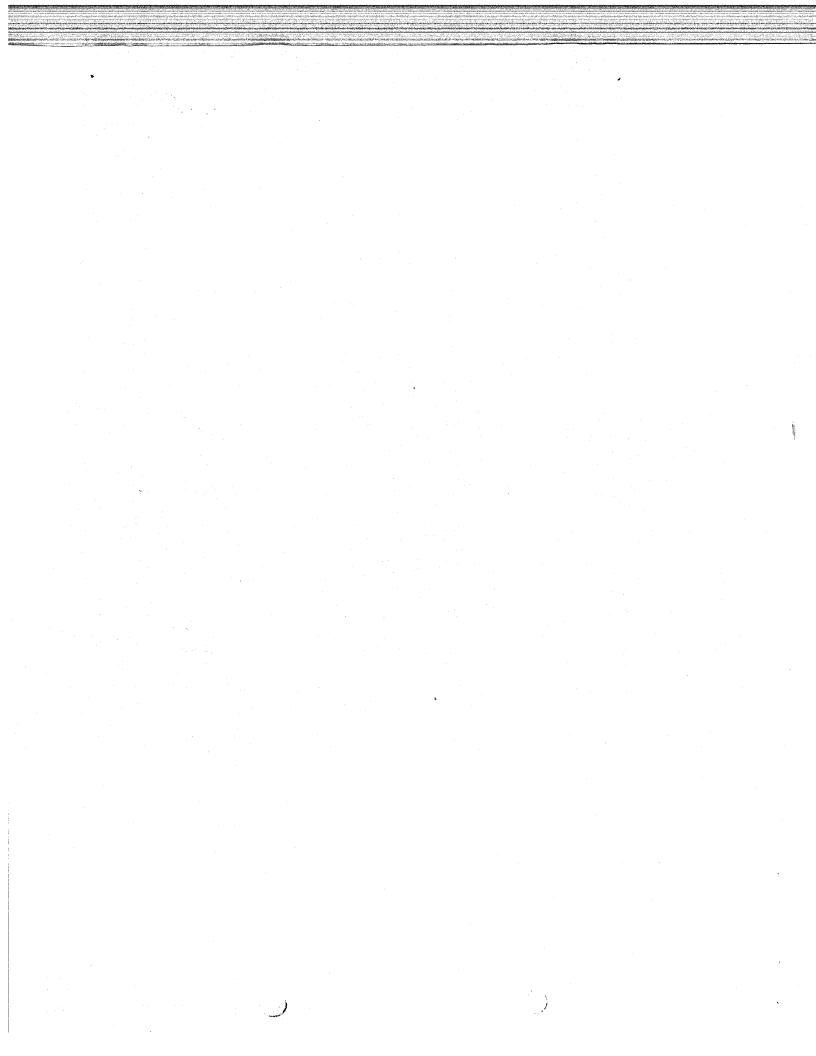
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                                                      APPLICANT: Lemischka, Ihor R.

IIILE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
IIILE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STEET: 180.VARICK STREET
                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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65.0%; Pred. No. 4.9e-210;
live 0; Mismatches 576;
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US92/05401
                   Sequence 5. Application PC/TUS9205401 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-
IELECOMMUNICATION:
IELEPHONE: 212-645-1405
                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
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NUCLEIC ACID
EDNESS: single
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INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGIH: 5405 base pairs
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30; Conservative
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MEDIUM TYPE: Floppy
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SOFIWARE: PatentI
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COUNIRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
PCI-US92-05401-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION:
PCT-US92-05401-5
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Matches 1080;
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2849 3326 2970 CCIAICAACIIAGGGGGCAAGAGAAAIGAAIIGIICCCIAIAAGAGCAAAGGGGC 3029 1217 9808 2429 2549 2610 TATIGTCAEGGATCCAGAEGAATIGCCCTIGGATGAGCGCIGTGAACGCTIGCCTIATIGT 2659 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 2850 GICTGAACTCAAGAICCICAICCACAIIGGICACCAICICAAIGIGGIGAACCICCIASG 2999 TCTGAGTGATGTTGAGGAAGAGGAGGATTCTGACGGTTTCTACAAGGAGCCCATCACAT 1337 1398 AAAGIGCAIICAICGGGACCIGGCAGCGAGAAACALICIIIIAICIGAGAACAAGCAAGGT 1458 GAAGATTTGTGATTTTGGCCTTGCCCGGGATATTTATAAGAACCCCGGATTATGTGAGAA 1517 2430 recordiceasascesascectoricalariasanssiscessesaaasseceasor 2489 1578 CAGCACCAAGAGGGACGIGIGGICTIACGGAGIAIIGCIGIGGGAAAICIICICCIIAGG 1637 191 801 858 GCCITITGGAAAAGIGGIICAAGCAICAGCAITIGGCAIIAAGAAAICACCIACGIGCCG 917 57.5 GGAGCTGATCACTCTAACATGCACCTGTGTGGCTGCGACTCTCTTGGCTCCTATTAAC CCICCITAICCGAAAAAIGAAAAGGIC---IICTICIGAAAIAAAGACIGACIACCIAIC AATTATAATGGACCCAGATGAAGTICCTTTGGATGAGCAGTGTGAGCGGCTCCCTTATGA TGCCAGCAAGTGGGAGTTTGCCCGGGAGACTTAAACTGGGCAAATCACTTGGAAGAG 918 GACTGTGGCTGTGAAAATGCTGAAAGGGGGCCCACGGCCAGGCGAGTACAAAGCTCTGAT 2790 AACAGIAGCCGICAAGAIGIIGAAAGAAGGAGCAACACACAGCGAGCAICGAGCCICAI 1098 TCTCTCCAACTACCTCAAGAGCAAACGTGACTTATTTTTTCTCAACAAGGATGCAGCAGT ACACATGGAGCCTAAGAAAAAAAATGGAGCCAGGCCTGGAACAAGGCAAGAAAACCAAG GGAAGAICIGAITICITACAGIITICAAGIGGCCAGAGGCAIGGAGIICCIGICIICAG GGGCTCTGTGGAAAGTTCAGCATACCTCACTGTTCAAGGAACCTCGGACAAGTCTAATGT 2490 1158 1278 1338 3207 551 621 681 738 198 978 501 > q g D D a ò g ò q P 음 g g g g δ ò òγ ò 台 g g ò 5 ò ò ò ò ò ó ŏ ద o. ò

3627 CIGGCAIGAGGACCCCAACCAGGAGACCTCGTTTTCAGAGTTGGIGGAGCATTIGGGAAA 3686 IGCCICCCCAIACCCIGGGGICAAGAIIGAIGAAGAATIIIGIAGGAGATIGAAAGAAGG CATGAGGATGAGAGCTCCTGAGTACTCTACTCCTGAAATCTATCAGATCATGCTGGACTG CISCACAGAGCCCAAAAGAAAGGCCAAGAITIGCAGAACTIGIGGAAAAACTAGGIGA 3587 CCICCIGCAAGCAAAIGCGCAGCAGGAIGGCAAAGACIAIA 3728 1818 IIIGCIICAAGCAAAIGIACAAGAGGAIGGIAAAGACTACAI 1859 1638 3507 1758 865E ŏ ó -G qq ó G. ò qq

Search completed: December 8, 2002, 12:53:53 Job time : 179.57 secs



Perfect sc Sequence:

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Database

Human flk-1 coding Fikl receptor prot Mouse fik-1 cDNA. Murine flk-1 recep Sequence of murine

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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AAA37816
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2000US-0649167.
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P-PSDB; ABG06099.
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                           WO200175067-A2
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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Human soluble vasc Nucleotide sequenc pD10-sFlt-1 vector

pTK gene SAL-S1. Protein tyrosine-k Bovine c-Kit bK-1

Human c-kit oncoge

New isolated polynucleotide and encoded polypeptides, useful in

Result No.

Nucleotide sequenc Human soluble VEGF

Soluble VEGF recep

sVEGF-RI gene.

Human tyrosine kin Plasmid pRK5.tkl-1

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mutations cs, forensics, gene mapping, identification of mutation le for genetic disorders or other traits and to assess Claim 1; SEQ ID No 5090; 103pp; English diagnostics, 

The invention relates to isolated polynucleotide (I) and polymerase chain reaction (FCR) primers, oligomets, and for chromosome conditions are chain reaction (FCR) primers, oligomets, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (FCR) primers as expressed sequence tags of identifying expressed genes. (I) is useful in gene therapy techniques of or identifying expressed genes. (I) is useful in gene therapy techniques of or seture normal activity of (II) or to treat disease states involving or a food supplement. (II) and its binding partners are useful in medical cannot state a series and as a food supplement. (II) and its binding partners are useful in medical cannot state as expressing (II). (I) and (II) are useful in medical cannot state and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in casponsible for genetic disorders or other traits to assess biodisersity and to produce other types of data and products dependent on DNA and and amino acid sequences. AASA117-AASA544 represent novel human condition, the sequence data for this patent did not appear in the printed sequence data for this patent did not appear in the printed of sequence data for this patent did not appear in the printed of a produce of the invention.

Sequence 7680 BP; 2279 A; 1661 C; 1739 G; 2001 T; 0 other;

at ftp.wipo.int/pub/published\_pct\_sequences.

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2019 180 240 120 Gaps 1900 TATAICACAGATGIGCCAAAIGGGTTICAIGTIAACTIGGAAAAAAGCCGACGGAAGGA TATATCACAGATGTGCCAAATGGGTTTCATGTTAACTTGGAAAAAATGCCGACGGAAGGA GAGGACCIGAAACIGICIIGCACAGITAACAAGIICIIAIACAGAGACGIIACIIGGAII TTACTGCGGACAGITAATAACAGAACAATGCACTACAGTATTAGCAAGCAAAAAATGGCC **ATCACIAAGGAGCACTCCATCACTCTTAATCTTACCATCATGAATGTTTCCCTGCAAGAT** Query Match 100.0%: Score 2101; DB 23; Length 7680; Best Local Similarity 100.0%; Pred. No. 0; Msmatches 2101; Conservative 0; Mismatches 0; Indels 0; 19 121 181 Q d ô Q ò Q ò

2319 2199 360 240 420 08 2380 CCAGGAAGCAGCACGTTTATTGAAAGAGTCACAGAAGAAGGATGAAGGTGTCTATCAC CAGAICACTIGGIIIAAAAACAACCACAAAAIACAACAAGAGCCIGGAAIIAIIIIAGGA CCAGGAAGCAGCACGTGTTATTGAAAGAGTCACAGAAGAGGATGAAGGTGTCTATCAC 541 IGCAAAGCCACCAACCAGAAGGGCICIGIGGAAAGIICAGCAIACCICACIGIICAAGGA 361 ACAGIGGCCAICCAGCAGTICCACCACTITAGACTGTCATGCTAATGGIGTCCCCGAGCCI 421 481 g ŏ Q ò g ò Op ōλ g ολ

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2979 2619 2799 2859 1020 1260 2559 2679 2739 GIGSTIAACCIGCIGGGAGCCIGCACCAAGCAAGGAGGCCCICIGAIGGIGAIIGIIGAA 1080 FACTGCAAATATGGAAATCTCTCCAACTACCTCAAGAGGAAACGTGACTTATTTTCTC 1140 3159 AAGGAGCCCATCACTÁIGGAAGAICIGAITICTIACAGITTICAAGIGGCCAGAGGCAIG 1380 3220 AAGGAGCCATCACTATGGAAGATCTGATTACTACAGTTTTCAAGTGGCCAGAGGCATG 3279 GAGTICCIGICTICCAGAAAGIGCATTCATCGGGACCTGGCAGCGAGAACATTCTTTA 1440 ICIGAGAACAACGIGGISAAGAIIIGIGAIIIIGGCCTIGCCCGGGAIAIITAIAAGAAC 1500 IIICAGGAAGATAAAAGICIGAGIGAIGIIGAGGAAGAGGAGGAITCIGACGGITICIAC 1320 GAGIICCIGICIICCAGAAAGIGCAIICAICGGGACCIGGCAGCAGCAAACAIICIIIIA 3339 096 780 840 006 CTCTTCTGGCTCCTALTAACCCTCCTTATCCGAAAAATGAAAAGGTCTTCTTGAAATA CICIICIGGCICCIATIAACCCICCIIATCCGAAAAAIGAAAAGGICTTCTGGAAAIA GAGTACAAAGCTCTGATGACTGAGCTAAAAATCTTGACCCACATTGGCCACCATCTGAAC AAATCACTTGGAAGAGGGGCTTTTGGAAAAGTGGTTCAAGCATCAGCATTTGGCATTAAG AAATCACCTACGTGCCGGACTGTGGCTGTGAAAATGCTGAAAGGGGGGCCACGGCCAGC GAGTACAAAGCTCTGATGACTGAGCTAAAAATCTTGACCCACATTGGCCACCATCTGAAC CAAGGCAAGAAACCAAGACTAGATAGCGTCACCAGCAGCGAAAGCTTTGCGAGCTCCGGC AAGACTGACTACCTATCAATTATAATGGACCCAGATGAAGTTCCTTTGGATGAGCAGTGT GAGCGGCTCCCTTATGATGCCAGCAAGTGGGAGTTTGCCCGGGAGAGACTTAAACTGGGC 2500 2560 ( 841 2920 2980 3340 7 1021 1081 661 721 2860 601 781 961 1141 1321 901 1201 3100 1251 1381 3280 1441 ò a B: QQ Db Q QQ 5 CP QQ og. ά Ġ 9 8 3 g  $0\bar{y}$ Q. g 8 G ò ð ö ô g 5 õ  $\dot{\circ}$ 

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Plasmodium, virus, viroid, cytokine, prion, antisense cligonucleotide,
cytostatic, virucide, protozoacide, antibacterial, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of a
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ementary oligoRNA having v
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complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides or oligoribonucleotides for antisense inhibition of gene expression usef e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                cytokine, Id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases stability and thus intracellular concentration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TATATCACAGAIGTGCCAAATGGGTTTCATGTTAACTTGGAAAAAATGCCGACGGAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAGGCACCTATGCCTGCAGGCCAGGAATGTATACACAGGGGAAGAAATCCTCCAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24; Length 4017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4017 BP; 1235 A; 915 C; 903 G; 963 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2097.8;
Pred. No. 0;
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Best Local Similarity
Matches 2099; Conserv
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des a novel receptor tyrosine kinase, at is expressed on human endothelial acular endothelial growth factor and it is implicated in clinical.

S isolated from a human umbilical vein contained from a human umbilical vein solated from a human endothelial vein littors where also Aav99850-53). The predicted differences from the previously from the previously from the previously from the previously from to Lys, 848 (Glu to Val) and 1347 tein predicted by computer modeling to tionality. The invention also relates combinant hosts which contain a DNA a DNA fragment encoding the without a membrane anchor second human KDR, and human mutant ofeins or fragments can be used in send agonists of human KDR (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rotein, KDR - useful e.g. to screen diseases involving neoangiogenesis ation, cancers
                                                              numan; signal transduction;
enessis; diabetic retinopathy;
lammation; rheumatoid arthitis;
Nypersensitivity; antagonist;
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Antagonists of XDP useful for treating diseases involving necanglogenesis e.g. diabetic retinal vascularization, cancers (e.g. brain, breast, etc.) and forms of inflammation e.g. rheumatrid arthritis, psoriasis, contact dermatitis and hypersensitivity reactions. The polynucleotides are useful to screen for KDR
                                                                                                                                                                                                                                                        Saps
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                                                                                                                                                                                                                                                                                     218 ICAIGAAIGIIICCCIGCAAGAIICAGGCACCIAIGCCIGCAGAGCCAGGAAIGIAIACA
                                                                                                                                                                                                                                                                                                                                                            278 CAGGGGAAGAAAICCICCAGAAGAAAGAAAITACAAICAGAGGAICAGGAAGCACCAIAC
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                                                                                       antagonists/agonists and for gene therapy (e.g. by introducing a gene portion encoding a RDR protein containing functional ligand binding and membrane anchoing moieties but not tyrosine kinase activity). They are also useful to measure levels of human KDR.
                                                                                                                                                                                                               Score 715.4; DB 20; Length 4071;
Pred. No. 8e-207;
0; Mismatches 561; Indels 6;
                                                                                                                                                                               Sequence 4071 BP: 1169 A; 894 C; 1027 G; 981 I; 0 other;
                                                                                                                                                                                                                34.1%;
                                                                                                                                                                                                                                 Best Local Similarity 65.5 Matches 1078; Conservative
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HIV: HCV: gene expression; oligoribonucleotide; tumour; pathosen;
Nium; virus; viroid; cytokine; prion; antisense oligonucleotide:
utic; virucide; protozoacide; antibacterial; ds.
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1115 ASAGCAAACGIGACTIATITITICICAACAAGGAIGCAGCACTACACATGGAGCCIAAGA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCCTIGCCCGGGATATITATAAGAACCCCGATTATGTGAGAAAAGGAGATACTCGACTTC 1534
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                                                                                                                                                                                                                                                Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired terminal bases
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1886 TTAAGAATGCATGCATGCAGGACCAAGGACTATGTCTGCCTTGCTCAAGACAGGAAGA 1945 2006 TCACAGGAAACCTGGAGAAICAGACGACAAGTATTGGGGAAAGCAICGAAGTCTCAIGCA 2065 2126 AAGACTCAGGCATTGTATTGAAGGATGGGAACCGGAACCTCACTATCCGCAGAGTGAGGA 2185 2186 AGGAGGACGAAGCCTCTACACCTGCCAGGCATGCAGTGTTCTTGGCTGTGCAAAAGTGG 2245 2246 AGGCATITITCATAATAGAAGGTGCCCAGGAAAAGACGAAACTIGGAAAICAITAITCTAG 2305 2306 TAGGCACGGCGGIGATIGCCAIGIICTICIGGCIACTICTIGICAICAICCIACGGACCG 2355 CAGCATACCTCACTGTTCAAGGAACCTCGGACAAGTCTAATCTGGAGCTGATCACTGTAA 637 CATGCACCTGTGTGGCTGCGACTCTTCTGGCTCCTATTAACCCTCCTTATCCGAAAAA 697 698 IGAAAAGGIC---ITCTICIGAAATAAAGACIGACTACCIAICAATIATAAIGGACCCAG 754 218 TCATGAAIGTTTCCCTGCAAGATTCAGGCACCTAIGCCTGCAGAGCCAGGAAIGIAIACA 277 Gaps 2066 CGCCATCTGGGAATCCCCCTCCACAGATCATGTGGTTTAAAGATAATGAGACCCTTGTAG 278 CAGGGGAAGAATCCTCCAGAAGAAATTACAATCAGAGATCAGGAAGCACCATACC TCCTGCGAAACCTCAGIGAICACACAGIGGCCATCAGCAGTICCACCACTTIAGACIGIC 398 AIGCIAAIGGIGICCCCGAGCCICAGAICACIIGGIIIAAAAACAACCACAAAAIACAAC AAGAGCCTGGAATTATTTAGGACCAGGAAGCAGCACGCTGTTTATTGAAAGAGTCACAG **AAGAGGATGAA**GGTGTGTATCACTGCAAAGCCACCAACCAGAAGGGCTCTGTGGAAAGTT 34.0%; Score 713.8; DB 24; Length 4044; 65.5%; Pred. No. 2.4e-206; Live 0; Mismatches 562; Indels 6; Matches 1077; Conservative Local Similarity Query Match 338 458 a ò q å ò g οχ g ò g ò g õ ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for inhibiting expression of a target gene (AB19165-AB19179) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand single-stranded sequent of 1-4 nt. The method provides single-stranded sequent of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known
                                                                                                                                                                                                                                                                                                                                                                                            Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3443 GTCAGAGACCCACGITITCAGAGITGGTGGAACAITIGGGAAAICTCTTGCAAGCTAATG 3502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 CAGGGGAAGAAAICCICCAGAAGAAAAITACAAICAGAGAICAGGAAGCACCAIACC 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1946 CCAAGAAAAGACAIIGCGIGGICAGGCAGCICACAGICCIAGAGCGIGIGGCACCACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 71-72; 104pp; German.
                                           1835 TACAACAGGAIGGIAAAGACIACAI 1859
                                                                         3503 CICAGCAGGATGGCAAAGACIACAI 3527
                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 97
                                                                                                                                                                                                               BP.
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Matches 1077;
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binding to a receptor protein complex comprising a vascular endothelial growth factor receptor-2 (VEGFR-2) receptor protein and a neuropilin-1
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                                                                              (NP-1) receptor protein. One method comprises introducing a sample comprising the compound to the receptor protein and allowing the compound to bind to the complex. Signaling through VEGFR-2 is enhanced in the presence of the NP-1 co-receptor. The methods of the invention can be used for identifying novel pro- and anti-anglogenic compounds. The present sequence represents the DNA encoding a human VEGFR-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 AIGCIAAIGGIGICCCCGAGCCICAGAICACTIGGIIIAAAAACAACCACAAAAIACAAC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAIGCACCIGIGIGGGIGCGACICICIICTGGCTCCIATTAACCCICCIIAICCGAAAAA 697
                                                                                                                                                                                                                                                                                      218 ICAIGAAIGTIICGCIGCAAGAIICAGGCACCIATGCCIGCAGAAGCCAGGAAIGIAIACA 277
                                   invention relates to determining whether a compound is capable
                                                                                                                                                                                                                                                                                                                                                                    TIAAGCGGGCCAATGGAGGGAACTGAAGACAGCTACTTGTCCATCGTCATGGATCAG
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                                                                                                                                                                                                                          22; Length 4225;
                                                                                                                                                                                            Sequence 4225 BP; 1204 A; 940 C; 1067 G; 1014 T; 0 other;
                                                                                                                                                                                                                        Score 713.8; DB 22;
Pred. No. 2.5e-206;
0; Mismatches 562;
 Example 1; Page 32-39; 82pp; English.
                                                                                                                                                                                                                          34.0%;
                                                                                                                                                                                                                                      Best Local Similarity 65.5
Matches 1077; Conservative
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3323 GGGIAAAGAIIGAIGAAGAAIITTGIAGGGGAITGAAAGAAGGAACIAGAATGAGGGCCC
                                                                                                                                                                                                                                                                                                       GCCTTGCCCGGGATATITATAAGAACCCCGATTATGTGAGAAAAGGAGATACTEGACTTC
                                                  3143 GCTTGGCCCGGGATATTATAAAGATCCAGATIATGTCAGAAAAGGAGATGCTCGCCTCC
                                                                                                              3203 CITIGAAATGGAIGGCCCCAGAACAATTTTTGACAGGGGACACAATCCAGAGIGACG
                                                                                                                                                            IGIGGICTIACGGAGIATIGCIGIGGGAAAICTICICCIIAGGIGGGICCATACCCAG
                                                                                                                                                                                                                          GAGTACAAATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGGCATGAGGATGAGAGCTC
                                                                                                                                                                                                                                                                                   CTGAGTACTCTACTCCTGAAATCTATCAGATCATGCTGGACTGCTGGCACAGAGACCCAA
                                                                                               CICIGAAAIGGAIGGCICCCGAAIDIAICIIIGACAAAAICIACAGCACCAAGAGCGACG
                                                                                                                                                                                                                                                                                                                                                  AAGAAAGGCCAAGATTTGCAGAACTTGTGGAAAAACTAGGTGATTTGCTTCAAGCAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining compounds which bind to a complex comprising vascular endothelial growth factor receptor-2 and Neuropilin-1 to provide superior pro- and anti-anglogenic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor protein, vascular endothelial growth factor receptor-2; VEGFR-2; neuropilin-1; NP-1; co-receptor: human; angiogenic: ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine kinase; vascular endothelial cell growth factors: tumour; diagnosing; monitoring; ss.
                  2795 GAGGGCCACTGATGTGGATTGTGGAATTCTGCAAATTTGGAAACCTGTCCACTTACCTGA
                                                                                                                  2972 GIAGCCAGAGCICAGCAGCICIGGAIITGIGGAGGAGAAGICCCICAGIGAIGIAGAAG
                                                                                                                                                                                                      AAGAGGAGGATTCTGACGGTTTCTACAAGGAGCCCATCACTATGGAAGATCTGATTTCTT
                                                                                                                                                                                                                   ACAGITICAAGIGGCCAGAGGCAIGGAGITCCIGICITCCAGAAAGIGCAIICAICGGG
                                                                                                                                                                                                                                                                             3092 ACAGCIICCAAGIGGCIAAGGGCAIGGAGIICTIGGCAICGCGAAAGIGIAICCACAGGG
                                                                                                                                                                                                                                                                                                                              ACCTGGCGCCACGAAATAICCICTTAICGGAGAAGAACGIGGITAAAATCIGIGACTTIG
                                                                                                                                                                                                                                                                                                                                                       GCCTTGCCCGGGATAITTATAAGAACCCCGATTATGTGAGAAAAGGAGATACTCGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                    GAGTACAAATGGATGAGGACTITTGCAGTCGCCTGAGGGAAGGCATGAGGATGAGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1775 AAGAAAGGCCAAGATTTGCAGAACTTGTGGAAAAACTAGGTGATTTGCTTCAAGGAAATG
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                                                                              2855 GGAGCAAGAAAIGAAITIGICCCCTACAAGACCAAAGGGGCACGAIICCGICAAGGGA
                                                                                                                                                      GCAGCGAAAGCTTTGCGAGCTCCGGCTTTCAGGAAGATAAAAGTCTGAGTGATGTTGAGG
                                                                                                                                                                                                                                                                                                     ACCTGGCAGCGAGAAACATTCTTTATCTGAGAACAACGTGGTGAAGATTTGTGATTTTG
                                                                                                                                                                                                                                                                                                                                                                               GCTTGGCCCGGGATATTTATAAAGATCCAGATTATGTCAGAAAAGGAGATGCTCGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                       CTCTGAAATGGATGGCTCCCGAATCTATCTTTGACAAAATCTACAGCACCAAGAGGGACG
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                                                     1115 AGAGCAAACGTGACTTATTTTTTCTCAACAAGGATGCAGCACTACACATGGAGCCTAAGA
                                                                                                       1175 AAGAAAAAIGGAGCCAGGCCIGGAACAAGGCAAGAAAGCAAGACIAGAIAGCGICACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A novel type III RIK gene - the KDR gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1835 TACAACAGGATGGTAAAGACTACAT 1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3572 CTCACCAGGATGGCAAAGACTACAT 3596
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This sequence represents a novel type III receptor tyrosine kinase gene. A labelled EcoRI-BamHI DNA segment derived from clone BTII1081.8 was used as a probe to rescreen a human endothellal cDNA library in the continuous probe of the gene from which the insert portion of BTII1081.8 is derived. A synthetic probe designed from undigorides 3297-3325 of BTII1081.8 is then used to isobate more a Tull length clones. One of the clones, designated BTIII200.2 is cloned into pBluescript KS and the synthetic oligonucleotide IGANGGGGG AIG GAG cloned, which contains the initial sequence Metally in the first two anno acids encoded by the KDR gene, forming BTIV140, which is then purified on a CSCI density gradient. This was sequenced, together with BIII1081.8, and BTIII129.5 to comprise the entire ORE of 4,068 nucleotides of the KDR gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARAGGAAACCIGGAGAAICAGAGGACAAGIAIIGGGGAAAGCAICGAAGICICAIGCA 2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2185 ASGAGGAGGCCTCTACACCIGCCAGGCATGCAGTGTTCTTGGCTGTGCAAAAGTGG 2245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1885 TIANGAAIGCAICCTIGCAGGACCAAGGAGCIAIGICIGCCIIGCICAAGACAGGAAGA 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1945 CONGRAMAGACATIGCGIGGICAGGCAGCICACAGICCINGAGCGIGIGGCACCCACGA 2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAIGCACCTGIGIGGGCIGCGACTCTTCTGGCTCCTATTAACCCTCCTTATCCGAAAAA 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TONIGNATGILICCCTGCAAGATICAGGCACCTAIGCCTGCAGAGCCAGGAATGIAIACA 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding type III receptor tyrosine kinase - useful diagnosing the onset of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4071 BP; 1172 A; 894 C; 1024 G; 981 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.8%; Score 710.6; DB 13 65.3%; Pred, No. 2.3e-205;
Location/Oualifiers
1..4058
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Matches 1075; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carrion ME, Terman BI;
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1115 AGAGCAAACGTGACITATTTTTTCTCAACAAGGATGCAGCACTACACATGGAGCCTAAGA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCTTGCCCGGGATATTTATAAGAACCCCGATTATGTGAGAAAAGGAGATACTCGACTTC-1534
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                                                                                               TIGCCCGGGAGAGTIAAACTGGGCAAATCACTTGGAAGAGGGGCTTTTSGAAAASTSG 874
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                                                                                                                                                                                                                                          GAGGGCCICTGATGGTGATTGTTGAATACTGCAAATATGGAAATCTCTCCAACTACCTCA
                                                                                                                                                                                                                                                 2726 GAGGGCCACTCATGTGTGTGGAATTCTGCAAATTTGGAAACCTGTCCACTTACCTGA
                                                                                                                                                                                                                                                                                                              AAGAAAAAIGGAGCCAGGCCIGGAACAAGGCAAGAAACCAAGACIAGAIAGGICACCA.
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                                                                                                                                                                                                                                                                                                                                                 1235 GCAGCGAAAGCITIGCGAGCICCGGCTTICAGGAAGAIAAAAGICIGAGIGAIGITGAG
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                          755 AIGAAGIICCTIIGSAIGAGCAGIGIGAGCGGCICCCIIAIGAIGCCAGCAAGIGGSAGI
                                                                                                                                875 IICAAGCAICAGCAIIIGGCAIIAAGAAAICACCIACGIGCCGGACIGIGGCIGIGAAAA
                                                                                                                                                                    TGCTGAAAGAGGGGGCCACGAGCAACAAAGCTCTGATGACTGAGCTAAAAATCT
                                                                                                                                                                                                       TGACCCACATIGGCCACCATCIGAACGIGGITAACCIGCIGGGAGCCIGCACCAAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                   1295 AAGAGGAGGATICTGACGGTTTCTACAAGGAGCCCATCACTATGGAAGATCTGATTTCTT
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1775 AAGAAAGGCCAAGATTTGCAGAACTTGTGGAAAAACTAGGTGATTTGCTTCAAGCAAATG 1834
                             3443 GICAGAGACCACGIIICAGAGIIGGIGGAACAIIIGGGAAAAICICIIGCAAGCIAAIG 3502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 CAGGGGAAGAAAICCICCAGAAGAAAGAAAITACAAICAGAGAICAGGAAGCACCAIACC 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinase insert domain containing receptor; KDR; screening; inhibitor; vascular endothelial growth factor; VEGF; angiogenesis; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening assay for vascular endothelial cell growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..4071
                                                                                                   1835 TACAACAGGATGGTAAAGACTACAT 1859
                                                                                                                              3503 CICAGCAGGAIGGCAAAGACIACAI 3527
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                                                                                                                                                                                                                                                                                  85
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97US-0810116.
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Matches 1075; Conservative
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1946 CCAAGAAAAGACAITGCGIGGICAGGCAGCICACAGICCIAGAGCGIGIGGCACCCACGA 2005	338 ICCTGCGAAACCICASIGAICACACAGIGGCCAICAGCAGIICCACCACIIIAGACIGIC 397 1	398 AIGCIAAIGGISCICCGAGCICAGAICACIIGGIIIAAAAAACAACACACAAAAIACAAC 457 	458 AAGAGCIGGAAITAITITAGGACGAGGAAGCAGGCIGITIAIIGAAAGAGICAGA 517 	518 AAGAGGAIGAAGGIGICIAICACIGCAAAGCCACCAACCA	578 CAGCAIACCICACIGIICAAGGAACCICGGACAAGICIAAICIGGAGCIGAICACICIAA 637 	638 CAIGCACCIGIGGGIGGGACTCTICTGGCTCCTATAACCCTCCTATCGAAAAA 697 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	698 TGAAAAGGTCITCITCIGAAAJAAAGACIGACTACCATCAAITAIAATGGACCCAG 754   11   1   1   1   1   1   1   1   1	755 ATGAAGIICCIIIGGAIGAGCAGIGIGAGCGGCICCCIIAIGAIGCCAGCAAGIGGGAGI 814   HIII   HIIIIII   HIIII   HIIIII   HIIII   HIIII   HIIII   HIIII   HIIII   HIIII   HIIII   HIIIII   HIIII   HIIIII   HIIII   HIIII   HIIII   HIIII   HIIII   HIIII   HIIIII   HIIII   HIIII   HIIII   HIIII   HIIII   HIIII   HIIII   HIIIII   H	815 TIGCCGGGGGAGAGACITAAACIGGGAAATCACITGGAAGAGGGCTITIGGAAAAGIGS 874 1	875 TICAAGCAICASCAITIGGCAITAAGAAATCACCTAGGTGCCGGACTGTGGAAAA 934 	935 IGCIGAAAGAGGGGCCACGCCAGCGAGIACAAAGCICIGAIGACIGAGCIAAAAATSI 994   1   1   1   1   1   1   1   1   1	995 TGACCCACATIGGCCACCATCTGAACGTGGTTAACCTGCTGGGGGCCTGCACCAAGCAG 1054	1055 GAGGGCTCTGATGGTGATTGTGAATACTGGAAATATGGAAATCTCTCCAACTACCTCA 1114   HILL   H	1115 AGAGCAAACGIGACITATITITICICAACAAGGAIGCAGCACTACACAGGGCCIAAGA 1174	1175 AAGAAAAAATGGGGGGGGGGGGAAGAAGGAAGAAGAGTGACGA 1234   H   H   H   H   H   H   H   H   H	1235 GCAGCGAAAGCITTGCGAGCTCCGGCTTTCAGGAAGATAAAAGTCTGAGTGATGTTGAGG 1294   H   H   H   H   H   H   H   H   H	1295 AAGAGGAGGATICTGACGGTITCIACAAGGAGCCCAICACIAIGGAAGATCIGATITCIT 1354   HILLI	1355 ACAGITICAAGIGGCCAGAGGCAIGGAGITCCIGICIICCAGAAAGIGCAIICAICGGG 1414 
qq ·	Oy Db	Qy Dp	Qy Db	Oy Ob	δ	Oy Db	Oy Db	Qy Db	Qy Db	Oy Db	Oy Db	07	0, 10	Oy Dp	Oy Db	Oy Dp	Oy Db	Qy Db

3383 CIGATIAIACTACACCAGAAAAGTACCAGACCATGCTGGACTGCTGGCACGGGGGAGCCCA 3442 3443 GTCAGAGACCCACGTITTCAGAGTTGGGGAACATTTGGGAAATCTCTTGCAAGCTAATG 3502 1083 ACCIGCGGCACGAAATAICCICIIAICGGAGAAGAAGGTGAAAATCIGTGACTTIG 3142 1555 GAĞTACAAATGGATGAGGACTİTTGCAGTCGCCTGAGGGAAGGCATGAGGATGAGAGCTC 1714 1323 GGGIAAAGAIIGAIGAAGAATIIGIAGGGATIGAAAGAAGAACIAGAAIGAGGGCCC 3382 1535 CICTGAAATGGATGGCTCCCGAATCTATCTTTGACAAAATCTACAGGCACCAAGAGCGACG 1594 1775 AAGAAAGGCCAAGAITIGCAGAACIIGIGGAAAAACIAGGIGAITIGCIICAAGCAAAIG 1834 1595 IGIGGICTIACGGAGIATIGCIGIGGGAAATCTICICCITAGGIGGGICICCATACCCAG 1654 1715 CIGAGIACTOTACICCIGAAAICIAICAGAICAIGCIGGACIGGCACAGAGACCCAA 1774 1415 ACCIGGCAGCAGAACAIICIIIIAICIGAGAACAACGIGGIGAAGAIIIGIGATIIIG 1474 Murine; foetal liver kinase 1; flk-1; protein tyrosine kinase; monoclonal, antibody; extracellular domain; receptor assay; hematopoictic stem cell: ligand; stimulation; proliferation; differentiation; readment; anemia; bone marrow damage; cancer chemotherapy; radiation; ds. Location/Qualifiers 208..4311 /\*tag= a 208..264 3503 CICAGCAGGAIGGCAAAGACTACAT 3527 1835 INCAACAGGAIGGIAAAGACTACAI 1859 Wirine foetal liver kinase 1 cDNA, BP. AAT38735 standard; cDNA; 5404 9205-0977451. 9105-0679666. 9105-0728913. 9105-0793065. 9105-0906397. 9205-0906397. 910S-0579666 /\*tag= b 265..4308 /\*tag= c (first entry) 19-NOV-1991; 02-APR-1991; 28-JUN-1991; 15-NOV-1991; 25-JUN-1992; 12-NOV-1992; Mus musculus 02-APR-1991: 11-DEC-1996 TS5548065-A sig\_peptide mat\_peptide 20-AUG-1995 AAT38735; Key

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2570 TGCCAGCAAGTGGGAATTCCCCAGGGACGGCTGAAACTAGGAAACCTTTGGCCGGGG
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                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes murine foetal liver kinase 1 (flk-1), a protein tyrosine kinase. Isolated antibodies, pref. moncolonal, raised against the extracellular portion of flk-1 can be used to assay for flk receptors on the surface of haematopoietic etem cells, and to isolate positive cells. The antibodies can also be used as, or to obtain ligands, which stimulate the proliferation and/or differentiation of stem cells. The ligands can be used, e.g. for treating anaemia, or bone marrow damage resulting from cancer
                                                                                                                                                                                                                     Anti-foetal liver kinase 2 (fik-2) antibodies - useful in assays, for isolating haematopoietic stem cells expressing receptor and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 TCAGGAAGCACCAIACCICCIGCGAAACCICAGIGAICACACAGIGGCCAICAGCAGIIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2190 GCGCATGGCACCCATGATCACCGGAGAATCTGGAGAATCAGACAACAACAACATTGGCGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACCACAAAATACAACAAGAGCCTGGAATTATTTTAGGACCAGGAAGCAGCACGCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.7%; Score 708.4; DB 17; Length 5404; 65.0%; Pred. No. 1.3e-204; Live 0; Mismatches 576; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5404 BP; 1411 A; 1297 C; 1423 G; 1273 T; 0 other
                                                                                                                                                                                                                                                                                                          Disclosure; Columns 51-62; 50pp; English.
  93US-0055269
94US-0252517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemotherapy, or radiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 1080; Conservative
                                                               (UYPR-) UNIV PRINCETON.
                                                                                                                                                     WPI; 1996-392678/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                  obtaining ligands
                                                                                                                                                                            P-PSDB; AAT38735
                                                                                                          Lemischka IR;
30-APR-1993;
31-OCT-1994;
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2849 1037 3387 AGGAGATGCCCGACTCCCTTTGAAGTGGATGGCCCCGGAAACCATTTTTGACAGGTATA 3446 3030 ACGCIICCGCCAGGGCAAGGACTACGTIGGG---GAGCICTCCGIGGAICTGAAAAGACG 3086 1698 CATGAGGATGAGAGCTCCTGAGTACTCTACTCCTGAAATCTATCAGATCATGCTGGACTG 1757 CIGGCACAGAGACCCAAAAGAAAGGCCAAGATTTGCAGAACTTGTGGAAAAACTAGGTGA 1817 TCTCTCCAACTACCTCAAGAGCAAACGTGACTTATTTTTTCTCAACAAGGATGCAGCACT 1157 1218 ACTAGATAGCGICACCAGCAGCGAAAGCTTTGCGAGCTCCGGCTTTCAGGAAGATAAAAG 1277 GICTGAACTCAAGATCCTCATCCACATTGTCACCATCTCAATGTGGTGAACTCCCTAGG 1278 TCTGAGTGATGTTGAGGAAGAGGAGTTCTGACGGTTTCTACAAGGAGCCCATCACTAT 1458 GAAGATIIGTGATITITGGCCTTGCCCGGGAIAFIFTATAAGAACCCCGATIAFGFGAGAAA CAGCACCAAGAGCGACGIGIGGICITACGGAGTAIIGCIGIGGGAAAICIICICCITAGG 1038 AGCCIGCACCAAGCAAGGAGGGCCTCTGATGGIGATTGTTGAATACTGCAAATATGGAAA 2910 CGCCTGCACCAAGCCGGGAGGCCTCTCATGGTGATTGTGGGAATTCTCGAAGTTTGGAAA ACACATGGAGCCTAAGAAAGAAAAATGGAGCCAGGCCTGGAACAAGGCAAGAAACCAAG GGAAGATCTGATTTCTTACAGTTTTCAAGTGGCCAGAGGCATGGAGTTCCTGTCTTCCAG 3207 GGAGCATCTCATCTGTTACAGCTTCCAAGTGGCTAAGGGCATGGAGTTCTTGGCATCAAG 3267 GAAGIGIAICCACAGGGACCIGGCAGCACGAACAIICICCIAICGGAGAAGAAIGIGGI 1638 IGGGTCTCCATACCCAGGAGTACAAATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGG GCCITITGGAAAAGTGGTICAAGCATCAGCATTTGGCATTAAGAAATCACCTACGTGCCG GACTGAGCTAAAATCTTGACCCACATTGGCCACCATCTGAACGTGGTTAACCTGCTGGG AAAGTGCATTCATCGGGACCTGGCAGCGAGAACATTCTTTTATCTGAGAACAACGTGGT GACTGTGGCTGTGAAAATGCTGAAAGAGGGGGCCCACGGCCAGCGAGTACAAAGCTCTGAT 1818 IIIGCIICAAGCAAAIGIACAACAGGAIGGIAAAGACIACAI 1859 3687 CCICCIGCAAGCAAATGCGCAGCAGGAIGGCAAAGACIAIAI

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1338 GGAAGAICIGAIIICIIACAGIIITCAAGIGGCCAGAGGCAIGGAGIICCIGITCITCCAG 1397
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         2490 GGAAGTCAIIAICCICGICGGCACIGCAGIGAIIGCCAIGIICIICIIGGCICCIICIIGI 2549
                                                                                                                                                                                                                                                                                                                                                                                                 2550 CATICTEGIACGGACCGTIAAGCGGGCCAATGAAGGGGAACTGAAGACAGGCTACTTGTC 2609
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                                                                                                                441 CAACCACAAAATACAACAAGAGCCTGGAATTATTTTAGGACCAGGAAGCAGCACGCTGTT 500
                                                                                                                                                                                                                                       GGGCTCTGTGGAAAGTTCAGCATACCTCACTGTTCAAGGAACCTCGGACAAGTCTAATCT 620
                                                    381 CACCACITIAGACTGICATGCIAATGGTGCCCCGAGCCTCAGATCACTTGGTTTAAAAA 440
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                                                                                                                                                                                              2370 INICECAGEGIGAGEAAGAAGAAGAAGAAGACCICIACAACCICCAGECCIGCAAGCTGAAAGTCCI
                                                                                                                                                                                                                                                                                                                                                                  CCICCIIAICCGAAAAAIGAAAAGGIC---IICIICIGAAAIAAAGACIGACIACCIAIC
                                                                                                                                                                             2430 TGGCTGTGCAAGAGGGGAGACGCTCTTCATAATAGAAGGTGCCCAGGAAAAGACCAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel method of isolating cells expressing fetal liver kinase 1 (flk.1) receptors on their surface and comprises binding the cells to a polyclonal or monoclonal antibody specific to antibody. The method can be used to isolate that have bound to the antibody. The method can be used to isolate hematopoietic stem cells in any mammal but preferably a rat, mouse, rabbit or human. The proteins of the invention belong to the receptor protein family. This sequence encodes the murine flk-1 protein which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2130 TGCTCAAGAIAAGAAGACCAAGAAAAGACATIGCCIGGTCAAACAGCTCAICAICCIAGA 2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 CACTCTTAATCTTACCATCATGAATGTTTCCCTGCAAGATTCAGGCACCTATGCCTGCAG 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20; Length 5404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolating hematopoletic cells expressing fetal liver kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5404 BP; 1411 A; 1297 C; 1423 G; 1273 T; 0 other;
                                                                                                                                          Murine; flk-2; flk-1; cell isolation; fetal liver kinase; monoclonal; polyclonal; antibody; tyrosine kinase; ds.
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65.0%; Pred. No. 1.3e-204;
. Wismatches 576;
                                                                                                                                                                                                                     Location/Qualifiers 208.4311 /*tag= a /product= "flk-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 59pp; English.
                     BP.
92US-0977451.
91US-0779666.
91US-073065.
91US-0813593.
92US-0906397.
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P-PSDB; AAY08618.
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Matches 1080; Conserv
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02-APR-1991;
28-JUN-1991;
15-NOV-1991;
24-DEC-1991;
26-JUN-1992;
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15-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACTCTTAATCTTACCATCATGAATGTTTCCCTGCAAGATTCAGGCACCTATGCCTGCAG 260
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                                                                                                                                                                                                                                                                                      Nucleic acid sequences coding for murine flk-2 and specified subfragments of it are claimed. The murine flk-1 coding sequence (i.e. AAQSSA) is also disclosed. The flk polypeptides are receptor protein tyrosine kinases which are expressed only in primitive haematopoletic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 708.4; DB 14; Length 5406;
Pred. No. 1.3e-204;
0; Mismatches 576; Indels 6;
                                                                                                                        Isolated nucleic acid molecules of hematopoietic stem cell receptor flk-2 - encoding mammalian receptor protein tyrosine kinases expressed in primitive haematopoietic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5406 RP; 1412 A; 1298 C; 1423 G; 1273 T; 0 other;
                                                                                                                                                                                                                                        English
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Best Local Similarity 65.0°
Matches 1080; Conservative
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                                                WPI: 1993-405021/50
                                                                          P-PSDB; AAR44996
Lemischka IR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1698 CATGAGGAIGAGGGCCCCTGAGTACTCTACTCCTGAAATCTATCAGATCATGCTGGACTG 1757
3326
                                                                                                                                                                                                              3387 AGGAGAIGCCCGACICCCIIIGAAGIGGAIGGCCCGGGAAACCAIIIIIGACAGGIAIA 3446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor protein tyrosine kinase; pIK family, foetal liver kinase; mflk; primitive; totipotent; haematopoietic cell; stem cell: proliferation; stromal cell; ds.
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                                                                                                                                                        3447 CACAATICAGAGCGAIGIGIGIGITICGITIGGCTCTGGGAAATATTTTCCTTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3627 CTGGCATGAGGACCCCAACCAGAGACCCTCGTTTTCAGAGTTGGTGGAGCATTTGGGAAA
3267 GAAGTGTATCCACAGGGACCTGGCAGCACGAAACAITCTCCTATCGGAGAAGAATGTGGT
                                                                                                                                                                                                                                                                     1578 CAGCACCAAGAGGGACGIGIGGICIIACGGAGIAIIGCIGIGGGGAAAICIICTCCIIAGG
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                                                   GAAGAITIGIGAITITIGGCCTIGCCCGGGAIAIIIAIAAGAACCCCGAITAIGIGAGAAA
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/note= "hydrophobic leader"
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910S-0728913.
910S-0793065.
920S-0906397.
920S-0975049.
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12-NOV-1992;
19-NOV-1992;
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28-JUN-1991;
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                                                                             ACACATGGAGCCTAAGAAAAAAAATGGAGCCAGGCCTGGAACAAGGCAAGAAACCAAG
                                                                                                                                                                          3030 ACGCIICCGCCAGGGCAAGGACIACGIIGGG---GAGCICICCGIGGAICIGAAAAAAA
                                                                                                                                                                                                                                                     ICTGAGTGATGTTGAGGAAGAGGAGGATTCTGACGGTTTCTACAAGGAGCCCATCACTAT
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                                  2850 GICIGAACICAAACACATCCACATIGGICACCATCICAAIGIGGGGAAACICCIAGG
                                                                  AGCCTGCACCAAGCAAGCAGGGCCTCTGATGGTGATTGTTGAAATACTGGAAAATAIGGAAAA
                                                                                                              1098 TOTOTOCOAACTACCTCAAGAGCAAACGTGACTTATITITICTCAACAAGGATGCAGCACT
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                       GACTGAGCTAAAAATCTIGACCCACATIGGCCACCATCTGAACGTGGTIAACCTGCTGGG
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This sequence encodes a human receptor protein tyrosine kinase which belengs to a new functional class of protein tyrosine kinases (prks). Elevers, this prix is not in the same class as flx-2. prks in the same class as flx-2 are expressed in primitive mammalian hematopoietic elass as flx-2 are expressed in primitive mammalian hematopoietic fis expressed in mature hematopoietic cells flwf). This gene is expressed in more mature hematopoietic cells. The protein encoded by this sequence is an example of a receptor prk and is called fetal liver spheen. Liver kinnes I (flx-1). flx-1 is expressed in fetal liver spheen. thymus, brain, stomach, kidney, lung, heart and intestine, and adult brain, kidney, heart, spleen, lung, muscle, marrow and lymph nodes.
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Human: receptor; protein; tyrosine kinase; pTK; primitive; mammalian; hematopoietic cell; pHC: mature: mHC; fetal; liver kinase 2: flk-1: liver; spleen; thymus; adult; brain; marrow; thymocyte; subset; multipotential; Tlymphoid; lineage; stomach; kidney; lung; heart; intestine; muscle; lymph node; ss.
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65.0%; Pred. No. 1.3e-204;
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Human flk-1 coding sequence

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receptor; protein; tyrosine kinase; pTK; flk-1; flk-2; adult; primitive; hematopoietic cell; mature; fetal; liver; spleen; brain; stomach; kidney; lung; heart; intestine; bone marrow; lymph node; ss
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                                                                                                      CIGGCACAGAGACCCAAAAGAAAGGCCAAGATTTGCAGAACTTGTGGAAAAAACTAGGTGA
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/note- "Hydrophobic leader sequence"
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                                               Length 5406;
                 Sequence 5406 BF: 1412 A; 1298 C; 1423 G; 1273 I; 0 other;
                                                                 0: Mismatches 575; Indels
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                                           33.7%; Score 708.4; DB 14 65.0%; Pred. No. 1.3e-204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATGAGGATGAGAGCTCCTGAGTACTCTACTCCTGAAATCTATCAGATCATGCTGGACTG 1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIGGCACAGAGACCCAAAAGAAAGGCCAAGATIIGCAGAACIIGIGGAAAAACIAGGIGA 1817
                                                                                                                                                                                                                                                          TCTGAGTGATGTTGAGGAAGAGGATTCTGACGGTTTCTACAAGGAGCCCATCACTAT
                                                                                                           GGAAGATCIGAITICTIACAGITTICAAGTGGCCAGAGGCAIGGAGTICCTGICTICCAG
                                                                                                                                                                AAAGTGCATTCATCGGGACCTGGCAGCGAGAACATTCTTTTATCTGAGAACAACGTGGT
                                                                                                                                                                                                                      AGGAGAIACICGACTICCICTGAAAIGGAIGGCICCCGAAICIAICTITGACAAAAICTA
                                                                                                                                                                                                                                                                                                                                                                       CAGCACCAAGAGGGACGIGIGGICTIACGGAGIAITGCIGIGGGAAAICTICICCTIAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                           /product = F1k1 receptor protein-tyrosine-kinase 208..264 /*rtag= b 255..4308 /*rag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Flk1; receptor protein-tyrosine-kinase; hematopoetic stem
cell; fetal liver kinase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flk1 receptor protein-tyrosine-kinase cDNA.
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2910 CGCCIGCACCAAGCCGGGAGGGCCICTCAIGGGAITGIGGAAITCICGAAGITIGGAAA 2969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1038 AGCTGCACCAAGCAAGGAGGCCTCTGATGGTGATTGTTGAATACTGCAAATATGGAAA 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3030 ACCTICCCCCAGGCCAAGGACTACGTTGGG---GAGCTCTCCGTGGATCTGAAAGACG 3086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1458 GAAGAITTGTGATTTIGGCCTIGCCCGGGATATTTATAAGAACCCCGATTATGTGAGAAA 1517
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TGCCAGCAGTGGGAATTCCCCAGGGACCGCTGAACTAGGAAAACTAGGCCGCGG
                                                                                                                                                                                                                                                             978 GACTGAGCIAAAAAICITGACCCACAIIGGCCACCAICTGAACGIGGIIAACCIGCIGGG
                                                                                                                                                                                                                                                                                1158 ACACATGGAGCCTAAGAAAAAAAATGGAGCCAGGCCTGGAACAAGGCAAGAAACCAAG
                                                  TGCCASCAAGTGGGGAGTTTGCCCGGGAGAGTTAAACTGGGCAAATCACTTGGAAGAGG
                                                                                                                      GGCIIIIGGAAAAGIGGIICAAGCAICAGCAITIGGCATTAAGAAATCACCTACGIGCCG
                                                                                                                                                                                         918 GACTGIGGCTGIGAAAAIGCTGAAAGAGGGGGCCCACGCCAGCCAGTACAAAGCTCTGAT
                                                                                                                                                                                                                   1278 TCTGAGTGATGTTGAGGAAGAGGAGGATTCTGACGGTTTCTACAAGGAGCCCATCACTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2190 GCGCAIGGCACCCAIGAICACCGGAAAICIGGAGAAICAGACAACAACAAIGGCGAGAC 2249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 AGCCAGGAAIGTAIACACAGGGGAAGAAAICCICCAGAAGAAAAAAAAITACAAICAGAGA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                        liver kinase) receptor protein-tyrosine-kinase. Flk1 is expressed in both primitive and mature hematopoietic cells, and in other tissues. The gene product is useful in isolation of receptor ligands, which have applications in diagnosis of bone marrow disorders and in stimulating proliferation and/or differentiation of primitive hematopoietic stem cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 TCAGGAAGCACCAIACCICCIGCGAAACCICAGIGAICACACAGIGGCCAICAGCAGIIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 CACCACTITAGACIGICAIGCIAAIGGIGICCCCGAGCCICAGAICACTIGGITIAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441 CAACCACAAAATACAACAAGAGCCTGGAATTATTTAGGACCAGGAAGCAGCAGGTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2550 CATICICGIACGACCGITAAGCGGGCCAATGAAGGGGAACTGAAGACAGCTACTIGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCTCTGTGGAAAGTTCAGCATACCTCACTGTTCAAGGAACCTCGGACAAGTCTAATCT
                                                                                                                                                                                                                                                                                                                                                                         sequence corresponds to a cDNA encoding a mouse Flk1 (fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 5406;
                                                                                                                                                                                                                                                                 Ligand for receptor protein tyrosine kinase - useful for the
                                                                                                                                                                                                                                                                                  stimulation of primitive haematopoietic stem cells causing proliferation and/or differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5406 BP; 1412 A; 1298 C; 1423 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         576; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.7%; Score 708.4; DB 16;
Similarity 65.0%; Pred. No. 1.3e-204;
30; Conservative 0; Mismatches 576;
                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 2: 131pp; English
                                        94WO-US05944
                                                                          93US-0080244
                                                                                        93US-0081508.
                                                                                                                                            (UYPR-) UNIV PRINCETON
                                                                                                                                                                                                               WPI; 1995-052014/07.
P-PSDB; AAR67817.
                                                                      18-JUN-1993;
21-JUN-1993;
23-NOV-1993;
                                                                                                                                                                                Lemischka IR;
                                     17-JUN-1994;
     05-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 1080;
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7 +51.6 21.5 566 14 BQ770907 AL570084 A	306 14.6 581 9 AA194109 303 14.4 496 10 AN129059 295.8 14.1 561 10 AN129059 296.8 14.1 9 623 12 BF081245 288.2 13.7 9 AA88012 288.6 13.4 819 9 AL570470 278.6 13.2 18.5 9 AL570470 277.6 13.2 10.67 14 BM92750 267.7 12.7 463 10 AN681286 267.7 12.7 463 10 AN681286 265.2 12.6 574 9 AL56889 265.2 12.6 574 9 AL56889 265.4 12.4 547 10 BE030679 259.6 12.4 320 9 ALIGNMENTS	RESULT 1 AKO04721 LOCUS AKO4721 LOCUS DEFINITION Mus musculus adult male lung cDNA, RIKEN full-length enriched likrary. clone:1200012822:FMS-like tyrosine kinase 1, full insert ACCESSION AKO04721 GI:15919895 KENWORDS HIC: CAP trapper SOURCE CLORE-LID:RIKEN full-length enriched mouse cDNA to mRNA, clone:1200012822. Clone:1200012822.	EUKATYOCA: Metazoa; Chordata; Craniata; Vertecrata; Euteleostomi; EUKATYOCA: Metazoa; Chordata; Craniata; Waridae; Murinae; Mus. 1111E AUTHOR. Carninol, P. and Hayashizaki, Y. 1111E High: efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) Hebris 9279233 FUBMED 10349636 REFERENCE Carninol, P., Shibata, Y., Hayatsu, N., Sugañara, Y., Shibata, K., Icoh, M., Koono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Ille Normalization and subtraction of cap-trapper-selected cDNAs to JOURNAI. Prepare full-length cDNA libraries for rapid discovery of new genes MEDRINE 20459374 PUBMED 11042189
Copy nucleic s Decemb Decemb THIS TOTAL TO	Maximum DB seq length: 0  Maximum DB seq length: 200000000  Post-processing: Maximum Match 100%  Listing first 45 summaries  Database: EST:*  1: em_estba:* 2: em_estba:* 3: em_esthum:* 4: em_estru:* 5: em_estru:* 6: em_estru:* 7: em_estro:* 8: em_inc:* 9: gb_estl:* 11: gb_htc:* 12: gb_estl:* 13: gb_estl:* 14: db_estl:* 14: db_estl:* 14: db_estl:* 14: db_estl:* 15: db_estl:* 16: db_estl:* 17: db_estl:* 16: db_estl:* 17: db_estl:* 17: db_estl:* 18: db_estl:* 18: db_estl:* 19: db_estl:* 10: db_estl:* 10: db_estl:* 10: db_estl:* 11: db_estl:* 12: db_estl:* 13: db_estl:* 14: db_estl:* 14: db_estl:* 15: db_estl:* 15: db_estl:* 16: db_estl:* 17: db_estl:* 17: db_estl:* 18:		Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.    SUMMARIES   SUMMARIES

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1. 3976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAB22504.2"
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/db_xref="MGD:MGI:55558"
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FGLARDIYKNPDYVRRGDTRLPLKWAAPESIFDKVYSTKSDVWSYGVLLWEIFSLGGS
PNEGYQMDEDFCSRLKEGMRMETPEPATPETYQIMLECHHKDPKERFRFAELVEKLGD
LLQANVQQDGKDYTPLNALLTRNSGFTYSTFFFSEDLFKDGFADFHFHSGSSDDVRYV
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LKĪĀSKSKEĀGLŠDLPRPSFCFSSCGHIRPVJDESELJKESCCSPFPDYNSVVLYSS
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           988 AAAAICIIGACCCACATIGGCCACCAICIGAACGIGGIIAACCIGGIGGGAGCCIGGACC 1047
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data source:MGD, source key:MGI:95555, evidence:ISS
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                                                                                                                                                   /organism-"Mus musculus"
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                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                              /db_xref="taxon:100
/clone="1200012B22"
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/gene="Flt1"
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                    Konno, H., Akiyama, J., Nishi, K., Kitsunai, I., Tashiro, H., Itch, M., Sumi, N., Ishi, Y., Nakhura, S., Mitsunai, I., Tashiro, H., Itch, M., Sumi, N., Ishiha, T., Harada, A., Yamamotto, R., Matsunoto, H., Sakayuchi, S., Ikegami, I., Kashiwaji, Yoneda, Y., Ishikawa, Y., Ishwa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, X., Tanaka, I., Matsunoto, K., Karai, J., Kashi, Y., Ishikawa, T., Ozawa, X., Tanaka, I., Matsunia, S., Karai, J., RIKEN integrated sequence analysis (RISA) system-jay-format Genome Res. 10 (11), 1757-1771 (2000)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                   1408 CATCGGGACCTGGCAGCGAGAAACAFTCTTTATCTGAGAACAACGTGGTGAAGATTTGT 1467
                                                                                1468 GALTITGGCCTTGCCCGGGATATITATAAGAACCCCGATTAIGTGAGAAAAGAAGIACI 1527
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                                                 1018 ATGAGCCTGGAAAGAATCAAAACCTTTGAGGAGCTTTCACCGAACTCCACCTCCATGTTT.1677
898 AGIGGCTTCACATACTCGACCCCCACCITCTCTGAGGACGCTIIGA 557
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                              GACCCAAAAGAAAGCCCAAGATTTGCAGAACTTGTGGAAAAACTAGGTGATTTGCTTCAA
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Tissue Procurement: Life Technologies, Inc.
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CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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Cole-Torgan: pooled colon, kidney, stomach: Vector:

"MV-SPORTE: Site_1: Not1: Site_2: cockv (destroyed); RNA-
source anonymous pool of 3 colons, age 26 yo male, 49 yo
famale, 71 yo male colon: 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo famale. Library is
clido-di primed and directicnally cloned (Bookv site is
destroyed upon cloning). Average insert size 1.4 kb.
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Close distribution: MGC clone distribution information can if found through the I.M.A.G.E. Consortium/LLNL at:
http://imag.llnl.gov.c.column: 24
High quairity sequence stop: 757.
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99.7%; Pred. No. 8.2e-192;
live 0; Mismatches 0;
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/clone="IMAGE:5188559"
/clone_lib="NIH_MGC_116"
/tab_host="DR10B"
                                                                                                                                          /organism="Homo sapiens"
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37, Conservative
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Standard POR techniques from stem-cell receptor-contg, tissue cDNA libraries. Suitable tissues include foetal liver, spleen or thymus cells or adult marrow or brain cells. The POR primers used are based on known sections of the flx-1 gene. The murine flk-1 clone may be known sections of the flx-1 gene. The murine flk-1 clone may be known sections of the flx-1 gene may be known sections of the flx-1 gene may be known sections of the fly manual be proposed in primative but not mature hammatapoietic cells. Ligand binding to the fx may be prepel, which hammatapoietic cells in vivo. The ligands can stimulate the proliferation and/or differentiation of primative proliferation of additional primitive stem cells, differentiation into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor protein tyrosine kinase; pTK family; foetal liver kinase; mflk; primitive; totipotent; haematopoietic cell; stem cell; proliferation; stromal cell; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 AGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                   Stimulating proliferation and/or differentiation of primitive mammalian haematopoietic stem cells - using ligand that binds thymidine kinase and flk-1 and flk-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5406;
                                                                                                                                                                                                                                                                                                                                                                                                                  The murine foetal liver kinase (flk) -1 clone was isolated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5406 BP; 1412 A; 1294 C; 1427 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 74.6; DB 13
Pred. No. 1.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               more mature progenitor cells, or both
See also AAQ29954-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= mflk-1
208..264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQS3504 standard; cDNA; 5406 BP
                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Fig 2; 94pp; English.
                                                                       91US-0679666.
91US-0728913.
91US-0793065.
91US-0813593.
                                       92WO-US02750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.8%;
78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 78.8 nes 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208..4311
                                                                                                                                                                     (UYPR-) UNIV PRINCETON
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                                                                                                                                                                                                                                           WPI; 1992-366185/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine flk-1 cDNA.
                                                                                                                                                                                                                                                                 P-PSDB; AAR28041
                                                                                           28-JUN-1991;
15-NOV-1991;
                                                                                                                                                                                                             Lemischka IR;
                                     02-APR-1992;
                                                                         02-APR-1991;
                                                                                                                                 24-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
15-0CI-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ53504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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AAQ53504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fetal liver kinase 1 (flk.1) receptors on their surface and comprises binding the cells to a polyclonal or monoclonal antibody specific to the FLK-1 receptor and isolating the cells that have bound to the antibody. The method can be used to isolate hematopoletic stem cells in any mammal but preferably a rat, mouse, rabbit or human. The proteins of the invention belong to the receptor protein family. This sequence encodes the murine flk-1 protein which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3395 CCCGACTCCCTTTGAAGTGGATGGCCCGGAAACCATTTTGACAGAGTATACACAATC 3454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel method of isolating cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 CTCGACTTCCTCTGAAATGGATGGCTCCTGAATCTATGTTTTGACAAAATCTACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thymidine kinase; TK; haematopoietic; stem cells; proliferation; differentiation; progenitor cells; foetal liver kinase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3455 AGAGCGANGTGTGGTCTTTCGGTGTGGTGCTCGGGAAATATTTCCTTAGGT 3507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 AGAGCGACGTGGTCTTACGGAGTATTGCTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                    Isolating hematopoietic cells expressing fetal liver kinase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5404 BP; 1411 A; 1297 C; 1423 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 74.6; DB 20;
Pred. No. 1.8e-13;
0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ29957 standard; .cDNA; 5406 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                             91US-0679666.
91US-0728913.
91US-0793065.
91US-0813593.
                                                                                                                                                                           92US-0975049.
93US-0055269.
94US-0252498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.8%;
78.8%;
                           98US-0021324
                                                                                                                                                                                                                                     96US-0601891
                                                             92US-0977451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89; Conservative
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                                                                                                                                                                                                                                                                       (UYPR-) UNIV PRINCETON.
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P-PSDB; AAY08618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            flk-1 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                     24-DEC-1991;
26-JUN-1992;
                                                                                                                                                                                                                                                                                                            Lemischka IR;
                         10-FEB-1998;
                                                                                                                                                                                             30-APR-1993;
31-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                 15-NOV-1991
                                                                                                                                                                               992
                                                                                                                                                                                                                                 15-FEB-1996
                                                             19-NOV-1992
                                                                                                   28-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-1993
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invention.

Query Match

Matches

ΩD ð

AAQ29957;

RESULT 12 AAQ2995

G.

receptors

12-NOV-

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This sequence encodes a human receptor protein tyrosine kinase which belongs to a new functional class of protein tyrosine kinases (pTKs). However, this pTK is not in the same class as fik-2. pTKs in the same class as fik-2. pTKs in the same class as fik-2 are expressed in primitive mammalian hematopoietic (pHC) cells but not in mature hematopoietic cells (mHC). This gene is expressed in more mature hematopoietic cells. The protein encoded by this sequence is an example of a receptor pTK and is called fetal liver kinase i (fik-1). fik-1 is expressed in fetal liver.spleen, thymus, brain, stomach, kidney, lung, heart and incestine, and adult brain, kidney, heart, spleen, lung, muscle, marrow and lymph nodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3355 CCCGACTCCCTTTGAAGTGGATGGCCCCGGAAACCATTTTGACAGAGTATACACAATTC 3454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 CTCCACTICCTCTGAAATGGATGGCTCCTGAATCTATCTTTGACAAAATCTACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor; protein; tyrosine kinase; pTK; ilk-1; flk-2; adult; primitive; iematopojetic cell; mature; fetal; liver; spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primitive; lemaropoletic cell; mature; feral; liver; spleen; brain; stomack; kidney; lung; heart; intestine; bone marrow; lymph node; sex
                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding receptor protein tyrosine kinase - allows development of ligands to stimulate proliferation and/or differentiation of mammalian haematopoietic stem cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3455 AGAGGAIGTGTGGTGTTGGGTGTGTGCTGGGAAATATITTCCTTAGGT 3507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 AGAGCGACGIGTGGICTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 74.6; DB 14; Length 5406;
Pred. No. 1.8e-13;
0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5406 BP; 1412 A; 1299 C; 1422 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Locatión/Qualifiers
208..4311
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E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ40916 standard; cDNA; 5406
                                                                                                                                                           91US-0793065.
91US-0813593.
92WO-US02750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.8%;
78.8%;
                                                                                                     92WO-US05401
                                                                                                                                         91US-0728913.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 78.8 es 89; Conservative
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208..264
/*tag= b
                                                                                                                                                                                                                                     (UYPR-) UNIV PRINCETON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine flk-1 cDNA.
                                                                                                                                                                                                                                                                                                                                 P-FSDB; AAR31377
                                                                                                                                                           15-NOV-1991;
24-DEC-1991;
02-APR-1992;
                                                                                                                                                                                                                                                                           Lemischka IR;
                                                                                                   26-JUN-1992;
                       WO9300349-A.
                                                                                                                                         28-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                               07-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-0CF-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cr.ymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 CICGACTICCICIGAAAIGGAIGGCICCIGAAICIAITGACAAAAICIACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; receptor; protein; tyrosine kinase; pTK; primitive; mammalian; hematopoletic cell; pHC; mature; mHC; fetal; liver kinase 2; flk-1; liver; spleen; thymus; adult; brain; marrow; thymocyte; subset; multipotential; T-lymphodid; lineage; stomach; kidney; lung; heart; intestine; muscle; lymph node; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid sequences coding for murine flk-2 and specified subfragments of it are claimed. The murine flk-1 coding sequence (i.e. AQS1504) is also disclosed. The flk polypeptides are receptor protein tyrosine kinases which are expressed only in primitive haematopoletic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3455 AGAGCGATGTGGGCTCTTCGGTGTTGCTCTGGGAAATATTTTCCTTAGGT 3507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules of hematopoietic stem cell receptor flk-2 - encoding mammallan receptor protein tyrosine kinases expressed in primitive haematopoietic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5406 BP; 1412 A; 1298 C; 1423 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.8%; Score 74.6; DB 14; 78.8%; Pred No. 1.8e-13; ive 0; Mismatches 24;
/note= "hydrophobic leader"
265..4308
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208..4311
/*tag* a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 60pp; English.
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910S-0793065.
910S-0813593.
920S-0906397.
920S-0975049.
920S-0977451.
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                                                                                                                                                                                     91US-0679666
                                                                                                                                                   910S-0679666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 78.8
Matches 89; Conservative
                                     /*tag=
                                                                                                                                                                                                                                                                                                                                       PRINCETON.
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1593-405021/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR44996
                                                                                                                                                                                                                                                                                                                                                                         Lemischka IR;
                                                                                                                                                                                                                                                                                                                                     (UYPR-) UNIV
                                                                                                                                               02-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                   02-APR-1991;
                                                                       US5270458-A.
                                                                                                                                                                                                         28-JUN-1991;
                                                                                                                                                                                                                                     24-DEC-1991;
               mat_peptide
                                                                                                           14-DEC-1993
                                                                                                                                                                                                                         15-NOV-1991
                                                                                                                                                                                                                                                             26-JUN-1992
                                                                                                                                                                                                                                                                               12-NOV-1992
                                                                                                                                                                                                                                                                                               19-NOV-1992;
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Key

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Gaps

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This sequence encodes the murine receptor protein tyrosine kinase (PTK), flk-1. This pTK is not in the same family as flk-2 (see also AA404091-15) as it is expressed in primitive hematopoietic cells and also in mature hematopoietic cells. flk-1 is expressed in fetal liver, spleen, thymus, brain, stomach, kidney, lung, heart and intestine and adult brain, bone marrow, kidney, heart, spleen, lung, muscle and lymph nodes.
                                                                                                                                                                                                                                                                                   Totipotent haematopoietic stem cell receptors, their ligands and DNA sequences - for treating anaemia(s) and bose marrow damage due to e.g. cancer chemotherapy or radiotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5406 BP; 1412 A; 1298 C; 1423 G; 1273 T; 0 other;
/note= "Hydrophobic leader sequence"
265..4308
/*tag= c
                                                                                                                                                                                                                                                                                                                                                Claim 14; Fig 2; 127pp; English.
                                                                                                                             92WO-US09893.
                                                                                                                                                         910S-0793065
                                                                                                                                                                                     (UYPR-) UNIV PRINCETON.
                                                                                                                                                                                                                                            WPI; 1993-182479/22.
P-PSDB; AAR37504.
                                                                                                                                                                                                                 Lemischka IR;
                                                                                                                           16-NOV-1992;
                                                                                                                                                       15-NOV-1991;
                                                                 WO9310136-A.
                                                                                             27-MAY-1993.
                       mat_peptide
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3455 AGAGGGATGTGTGTGTGTGTGTGTGTGTGGGAAATATTTCCTTAGGT 3507

129 AGAGGGACGTGTGGTCTTACGGAGTATTGCTGGGAAATCTTCTCCTTAGGT 181

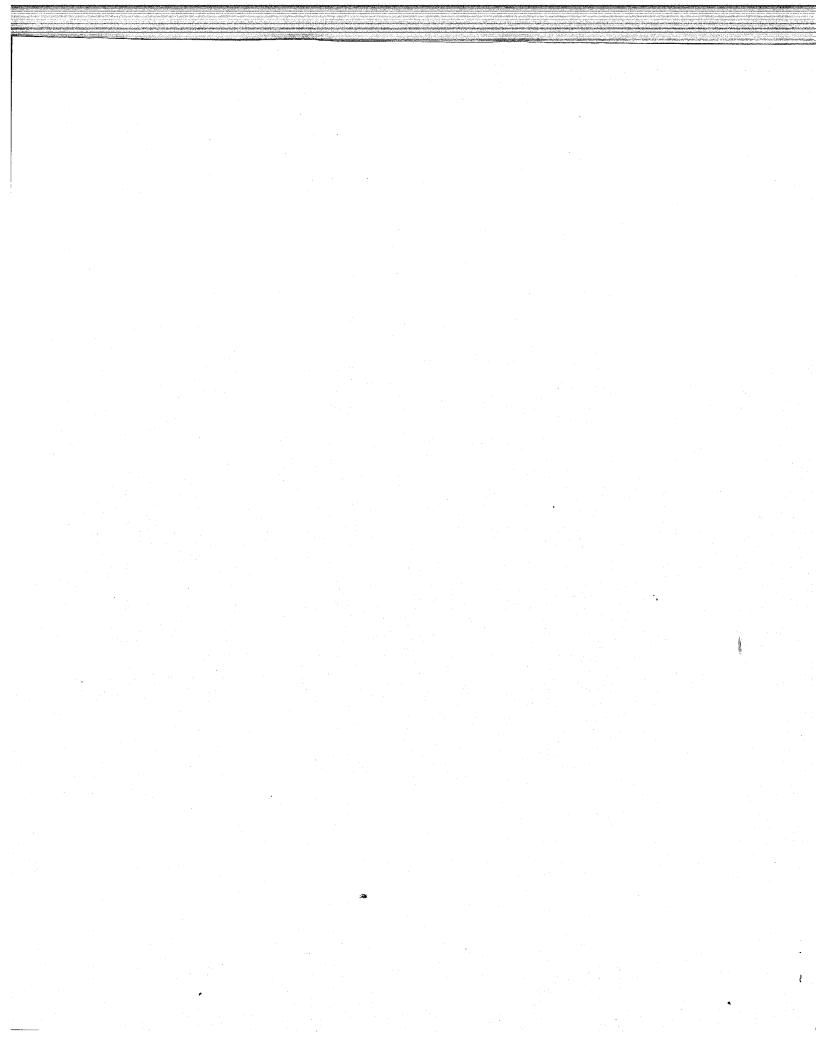
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Gaps

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Ouery Match 24.8%; Score 74.6; DB 14; Length 5406; Best Local Similarity 78.8%; Pred. No. 1.8e-13; Matches 89; Conservative 0; Mismatches 24; Indels 0;



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oM nucleic – nu	OM nucleic - nucleic search, using sw model	
Run on:	December 8, 2002, 05:16:46; Search time 2350.03 Seconds	
	(Without Ainguments) 3665.203 Million cell updates/sec	
Title:	US-09-778-900A-3_COPY_200_500	
Suguence:	1 ggacactcgggttgaatgtgtaacaaaaactcttaaagt 301	
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
Searched:	2054640 seqs, 14551402878 residues	
tal number of	tal number of hits satisfying chosen parameters: 4109280	
Minimum DB seq	Minimum DB seq length: 0	
Sost-processing	Fost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Databāse :	GenEmbl:* 1: qb_ba:*	

1: 9b htg:\*

2: 9b htg:\*

4: 9b\_ov:\*

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19: em\_ov:\*

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27: em\_in:\*

28: em\_in:\*

38: em\_itg\_in:\*

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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umber of results predicted by chance to have a

em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htgo\_other:\*

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/note="141257x repeat: matches 75. 133 of consensus" 27339. 27650
27359. 27650
27679. 27810
/note="Single clone region. Sequence from reads from a Short insert library derived from a single pUC clone. Sextiction digest data confirm the assembly."
                                                                                                                                                              .6169 of consensus
                                                                                                                                                                                                         .5477 of consensus
                                                                                                                                                                                                                                                                                                                                       repeat: matches 3892. .4063 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                       .5255 of consensus
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                     /note="L1M4 repeat: matches 4612. .47.06 of consensus"
12550. .12859
                                                                                                              matches 4344. .4612 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             //coce="Allub repeat: matches 144. 255 of consensus" 18089. 18379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89. .305 of consensus!
                                                                                                                                                                                                                                                                                                 30. .301 of consensus™
                                               12550. 12859
Gote-*AluSg repeat: matches 1. 310 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSx repeat: matches 1. 352 of consensus" 17794. 17914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #Alusq repeat: matches 1. .252 of consensus* 8380. .18516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="AluJb repeat: matches 1. .144 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Alusx repeat: matches 1. .268 of consensus" 26437. 26754
cote="MESZ repeat: matches 2. .311 of consensus" 28645. .27004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .297 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .160 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="11 copies 2 mer tt 100% conserved"
21313. .21486
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/note="charlie3 repeat: matches 48. .215.

25374. 25537

/note="82 copies 2 mer ta 61% conserved"

25538. .25830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 1. 251 of 24957. 25516
/note="Sequence from clone PCR only."
                                                                                                                                                    /note="LiMB7 repeat: matches 5629.
13789. 14015
/note="LiMB7 repeat: matches 5250.
                                                                                                                                                                                                                                     dole-"LIMA4 repeat: matches 4063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="LIMEc repeat: matches 1622.
7915. .18088
                                                                                                                                                                                                         repeat: matches 5250.
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29773. 29973
/note="MIR repeat: matches 37.
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27014. 27230
27014. Alusg/x repeat: matches
27233. 27286
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21878. 22123
                                                                                                                                                                                                                                                                                                    repeat: matches
                                                                                      /note="LIM4 repeat:
13227, 1374^
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17160. .17462
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/6507. .16680
                                                                                                                                                                                                                                                                                                                            /note="LIMA4 1
16689. .1fo+
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/note="llMA4">
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                                                                                                                                                                                                                                                    regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subochone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL, Sw. SWISSPROT; Tr., TREMBL, WP., WORMPEPP; Information on the WORMPEPP there is the control of the WORMPEPP.
                                                                                                                                      together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.
                                        requests: clonerequest8sanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:14715292.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/HGP/Chr13
RP11-502P18 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
Submitted (03-AUG-2001) Sangèr Centre, Hinxton, Cambridgeshire.
CBIO 18A, UK. E-mail enquiries: humqueryésanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sections only once, except for a 100 base overlap.
The true right end of clone RPI1-502718 is at 164519 in this sequence. The true lead of clone RPI1-5566 is at 120266 in this sequence. The true right end of clone RPI1-179F17 is at 2000 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             989. 2053

Oncle-"Alu/FLAM repeat: matches 21..86 of consensus" 7724. 2892

Thote="L2 repeat: matches 2206. 2358 of consensus" 732. 3435

Thote="L2 copies 2 mer ac 93% conserved" 7343. 3343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMPORTANT: This sequence is not the entire insert of clone RP11-502P18 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4495. 4586
/note="FlAM_C repeat: matches 33. .124 of consensus"
6847. 6934
/note="44 copies 2 mer ca 75% conserved"
8691. -9005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  634. .1706
note="MBR5A repeat: matches 95. .168 of consensus"
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note="Alusx repeat: matches 1. .297 of consensus"
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/note="AluSg repeat: matches 1, .307 of consensus"
12456. 12549
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Anote- U6 repeat: matches 2. .104 of consensus*
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/organism="Homo sapiens"
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/clone_lib="RPCI-11.2"
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sequences, will become prior art. Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the According to the Pre Publication Rules, every patent application received by the United States

extension .rnpb Published Applications NA contains nucleic acid sequences; the search results will have the Published\_Applications\_AA contains amino acid sequences; the search results will have the Two new databases have been created to hold the pre-published sequences:

extension .rapb.

digits represent when the application was published. This 7-digit number starts at zero at the application had been published. If the applicants submit changes to the application, they may beginning of each calendar year. Each application published is given the next number in order application. The first 4 digits show the calendar year the application was published. The next 7 Publication Number is US20021234567A1. The "US" indicates the application was a U.S. requests that the changed application be published again. In such instances, the "1" at the end of Each pre-published application is given a unique Publication Number. An example of a the number would be replaced by a "2" The "A" indicates a utility patent application and the "1" shows that this was the first time the

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.

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1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*

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Copyright (c) 1993 - 2002 Compugen Ltd.
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Ouery Match 5.6%; Score 52.6; DB 10; Length 1064; Best Local Similarity 41.5%; Pred. Nc. 0.0047; Matches 154; Conservative 0; Mismatches 217; Indels 0;

3950, Ap 99, App 40, App 40, App 8, Appl 8, Appl 1120, Ap 1120, Ap 1120, Ap 1121, Appl 3114, Appl 4, Appl 5, Appli 6, Appli 16, Appli 17, Appli 18, A	APP11 APP1 APP1 700, AP 76, APP	
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APPLICANT: Young, Paul
TILE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
TILE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DAIE: 2001-09-18
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530 CICGICGCCCCCCCTCTCCGIAGCCGCAGGGAAGCGACCTGGGAGGAAGAAGAGG 579
                                                            288 CAGGGCAGTGCCGGGGGGGGGGGTATGCCTCAGCCGGCGGCGGC 347
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Pred. No. 0.02;
0; Mismatches 259;
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PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
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PRIOR FILING DATE: 2000-09-26
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PRIOR PELING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR PRIOR DATE: 2000-09-27
PRIOR PRILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR PRIOR DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
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PRICE FILING DATE: 2000-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 292, Application US/09954456 Patent No. US20020115057A1 GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 43058
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APPLICANT: KOOPMAN, Peter Anthony
APPLICANT: MUSCAT, George Eugene Orlando
VIILE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES AND METHODS OF USING THEM
FILE REFERENCE: 21415-0003
CURRENT APPLICATION NUMBER: US/09/814,777A
CURRENT FILING DATE: 2001-03-23
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48.0%; Pred. No. 0.0092;
tive 0; Mismatches 191; Indels 3;
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US-05-814-77A-17
US-05-814-777A-17
Sequence 17, Application US/09814777A
Patent NS. USSO020142415A1
GENERAL INFORMATION:
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PRIOR AFPLICATION NUMBER: AU PQ6457
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 128
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CHER INFORMATION: Intron 1
NAME/KEY: misc_feature
LOCATION: (670
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NAME/KEY: misc_feature
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CIHER INFORMATION: Exon
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NAME/KEY: CDS
FORMTION: (679)..(1473)
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GRGANISM: Human
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US-09:814-777A-17
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NAME/KEY:
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453 GGGGCGGCGCTCCCGGGCCCGCGTCGCCACCTCCCCACGCGCGCTCGGCCCCGGGGCC 512
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                                                                                                                                                                                                                                                                                                       633 GGIGCCGGGGGTAGGAAGTGGGCIGGGGAAAGGTIATAAAICGCCCCCGCCCCCGGCTGCT 692
                                                                                                                                                                                                                                                                                                                                                                               693 CITCAICGAGGICCGCGGGAGGCICGGAGCGCGCGACACICCICICGGGICCIC 752
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 Score 50.6; DB 10; Length 43058; Pred. No. 0.02; 0; Mismatches 255; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 43058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INCOGRATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Useeph G.
APPLICANT: Scherf, User Gancer, ITLE OF INVENTION: Gene Expression Profiles in Liver Cancer, ITLE OF INVENTION: Gene Expression Profiles in Liver Cancer, FILE PEFERENT 44921-5028-WO.
CURRENT FILING DATE: 2001-06-14
PRICE APPLICATION NUMBER: US 60/211,379
PRICE PRICE DATE: 2000-06-14
PRICE PRICE PRICATION NUMBER: US 60/211,379
PRICE PRICE PRICE DATE: 2000-06-14
PRICE PRICE PRICE DATE: 2000-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Genbank Accession No. US20020142561A1 284721
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46.6%; Pred. No. 0.02;
Live 0; Mismatches 255;
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Patent No. US20020142981A1
 5.48;
                                         Conservative
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SOFIWARE: Patentin Ver. 2.1
SEQ ID NO 3950
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Best Local Similarity 46.65
Matches 228; Conservative
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ORGANISM: Homo sapiens
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25778 GGTCGCGGG 25786
Query Match
Best Local Similarity
Matches 228; Conserv
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US-09-880-107-3950
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TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
                               15359 ACCOGCAGACCAAGACCIACTICCCGC-ACTICGACCTGCACCCGGGGTCCGCGCAGTG 25417
                                                                                                         25418 CGCGCGCACGCGCCGAAGGTGGTGGCGCGCGGTGAAGAGCATCGACGAC 25477
                                                                                                                                                                                 25478 ATCGGGGCCCTGTCCAAGCTGAGGAGCTGCACGCTACATCCTGCGGGGGGCCCG 25537
                                                                                                                                                                                                                                                     693 CITCATCGAGGTCCGCGGGAGGCTCGGAGCGCGCCAGGCGGACACICCTCGGCTCCTC 752
                                                                                                                                                                                                                                                                                                           753 CCGGGAGGGGGGGGGGTCGGAGCGGGCTCGGGGTGCAGGGGCCAAGGGGGCG 812
     513 ACCCGCCCTCGTCGGCCCCCCCCTCTCCGTAGCCGCAGGGAAGCGAGCCTGGGAAGAA 572
                                                                               573 GAAGAGGTAGGTGGGGAGGCGGATGAGGGGTGGGGGACCCCTTGACGTCACCAGAAGGA 632
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR PELINO DATE: 2000-09-26
PRIOR PELINO DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR PELINO DATE: 2000-09-27
PRIOR PELINO DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
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PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
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PRIOR FILING DATE: 2000-09-27
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Patent No. US20020115057A1
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SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-954-456-529
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APPLICANT: Young, Paul
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US-09-954-456-529
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ZIP: 92122
COMPUTER READABLE FORM:
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Matches 100; Conservative
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                                                                                                                                                                                                             HYPOTHETICAL: NO
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COUNTRY: USA
                                                        TELEPHONE
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US-10-125-767-17/c
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TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL PHROMOSOMES
25359 ACCCGCAGACCAAGACCTACTTCCCGC-ACTTCGACCTGCACCCGGGGTCCGCGCAGTTG 25417
                                                                                                                                                                                    25418 CGCGCGCACGCCTCCAAGGTGGCCGCCGTGGGCGTGAAGAGCATCGACGAC 25477
                                                                                                                                                                                                                                                                                                                                                                           513 ACCCGCCTCGTCGGCCCCCCCCTCTCCGTAGCGCAAGCGAAGCGAGCCTGGGAAG 572
                                                                                                                                                               633 GGTGCCGGGGTAGGAAGTGGGCTGGGGAAAGGTTATAAATCGCCCCCCGCCCTCGCCTGCT 692
                                                                                                                                                                                                                          693 CTICATCGAGGICCGCGGGAGGCTCGGAGCGCCAGGCGGACACICCTCTCGGCICCIC 752
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                                                                                                                                                                                                                                                                                                                                                                                                         873 GCTCAGGGCGCGGCGGCGGCGGCGAACGAGGACGGACTCTGGCGGCCGGGTCTTT 932
                                                                                                   573 GAAGAGGTAGGGGGAGGCGGATGAGGGTGGGGGACCCCTTGACGTCACCAGAAGGA
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ADDRESSEE: Heller Ehrman White & McAulliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/799,462A
FILING DATE: 10-Sep-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/835,682
FILING DATE: 10.APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
FILING DATE: 12-UL-1996
FILING DATE: 12-UL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 110-APR-1996
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SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hadlaczky, Gyula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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US-09-799-462A-17/c
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389 GAGCCCGATGGGCAJJAGGAGGGGCAAGGGCAAGAGGGCGCGGAAGAAGACCCTGAACC 448
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Patent No. US20020160410A1
GENERAL INFORMATION:
APPLICANT: Hadlaczky, Gyula
ITILE OF INVENTION: ARITERIAL CHROMOSOMES, USES IHEREOF AND
METHODS
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Pred. No. 0.059;
0; Mismatches 86; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE LUDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe LLP
STREET: 4350 La Jolla Village Drive, 7th Floor
REGISTRATION NUMBER: 33,779
REFERENCE/GREET NUMBER: 24601-402G
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FASTSEQ Version 1.5
CURRNI APPLICATION DATA:
APPLICATION NUMBER: US/10/125,767
FILING DATE: 17-Apr-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/724,693
                                                                                                                                                                                                                                                                                                   FRACHENT TYPE: «Gnknown»
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17;
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APPLICATION NUMBER: 08/835,682
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APPLICATION NUMBER: 08/695,191
FILING DAIE: 07-AUG-1956
                                                                                                                                                              LENGIH: 42999 base pairs
                                                              TELEPHONE: 858-450-8403
TELEFAX: 858-587-5360
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                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: Senomic DNA
                                                                                                      TELEX: <Unknown>
INFORMATION FOR SEQ 15 NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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673 GGCCCCCGCCTCGCTTCTTCATCGAGGTCCGCGGAGGCTCGGAGCGCCCAGGCG 732
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APPLICANT: Lees, Simon M.
APPLICANT: Law, Simon M.
APPLICANT: Law, Simon M.
APPLICANT: Aljona, A.Lital A.
APPLICANT: Aljona, A.Lital A.
TILLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCIEROSIS
FILE REFERENCE: 107-0044001
CURRENT APPLICATION NUMBER: US/10/023,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           792 GGGTGCAGGGCCAGGGGGCGCCTGGCGGCAGGATTACCCGGGGAAGTGGTTGTCTCT
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Pred. No. 0.084;
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Pred. No. 0.084;
0; Mismatches 125; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFIWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 48 LENGTH: 2561
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PRIOR FILING DATE: 2000-07-14
PRIOR PLING DATE: 2000-03-02
PRIOR PLING DATE: 2000-03-02
PRIOR PLING DATE: 159-11-26
PRIOR APPLICATION NUMBER: US 08/979, 608
PRIOR FILING DATE: 159-11-26
PRIOR APPLICATION NUMBER: US 60/031, 930
PRIOR PLING DATE: 199-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 53
SCOTHARR: FASICEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 2561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/048,547 PRIOR FILING DATE: 1597-06-03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Sequence 48, Application US/10023523 ; Patent No. US20020152485A1
                                                                                                         ORGANISM: Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryctolagus cuniculus
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53.18
18.18
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                                                                                                                                                                                                                                                                                       Best Local Similarity 53.19
Matches 144; Conservative
                                                                                                                                                        ) NAME/KEY: CDS
: LOCATION: (246)...(1895)
US-10-023-529-48
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: LOCATION: (246)...(1895)
US-10-023-523-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
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                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                      FEATURE
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, SImon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
TITLE OF INVEWION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVEWION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVEWION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVEWION: PROTEINS AND THER COCCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 09/517,845
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1900-03-11-26
PRIOR FILING DATE: 1996-11-26
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   509 GGCCACCCGCCTCGTCGGCCCCCCGCCCTCTCCGTAGGCGCAGGGAAGCGAGCCTGGGA 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.1%; Score 48 4; DB 9; Length 42999; Best Local Similarity 53.8%; Pred. No. 0.059; Matches 100; Conservative 0; Mismatches 86; Indels 0;
                                                                                              AITORNEY/AGENT INFORMATION:
NAME: Seldman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-4023
TELECOMMUNICATION INFORMATION:
TELEPHANE: 858-450-8403
TELEPHAX: 858-587-5360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: <Unknown>
SOUGHAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-125-767-17
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
                                                                                                                                                                                                                                                                    TELEX: <Urknown>
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4299 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/10023529
Parent No. US200219388A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
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IIILE OF INVENTION: FROIEINS AND THEIR USE IN DIACKSING AND IREATING
IIILE OF INVENTION: A.HEROSCLEROSIS
FILE REFERENCE: 10997-004001
CURRENT APPLICATION NUMBER: 08/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR PELLYA DATE: 200-07-14
PRIOR PELLYA DATE: 200-07-14
PRIOR PELLYA DATE: 200-07-14
PRIOR PELLYA DATE: 1090-03-02
PRIOR PELLYA DATE: 1090-03-02
PRIOR APPLICATION NUMBER: US 09/519,608
PRIOR PELLNG DATE: 1997-11-26
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PRIOR PELLNG DATE: 1997-11-26
PRIOR PELLNG DATE: 1997-11-27
PRIOR PELLNG DATE: 1997-11-27
PRIOR PELLNG DATE: 1997-11-27
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Pred. No. 0.21;
0; Mismatches 230; Indels
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Sequence 45, Application US/10023523

Patent No. US20020152485A1

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon M.
APPLICANT: Axion M.
APPLICANT: Axion Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)...(1614)
US-10-023-529-45
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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LENGIH: 1614
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                                                                 Gaps
                                      673 GECCCCCCCCCTCGCTGTTCATCGAGGTCCGGGAGGCTCGGAGCGCGCCAGGCG 732
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                                                                                                                                                                                                 792 GGGTGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATTACCCCGGGGAAGTGGTTGTCTCCT
                                                                                                                                                                                                                        APPLICANT: Craig H. Day
APPLICANT: Craig H. Day
APPLICANT: Craig H. Day
APPLICANT: Davin C. Dillon
APPLICANT: Mocowan, Patrick
APPLICANT: Mocowan, Patrick
APPLICANT: Mocowan, Patrick
APPLICANT: Mocowan, Patrick
APPLICANT: Mocowan, Patrick
APPLICANT: Mocowan, Patrick
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
CURRENT APPLICATION NUMBER: US/09/894,998
CURRENT FILING DAYE: 2001-06-28
NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0
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      Indels
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1221 CCCCGACGACTGCCACACCCCCCCGGGGCCCGAG 1182
      Mismatches 125;
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Pred. No. 0.11;
0; Mismatches 71;
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Patent No. US20020090610A1
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Patent No. US20020129388A1
GENERAL INFORMATION:
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Best Local Similarity 55.6%;
Matches 89; Conservative (
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APPLICANT: Hosken, Nancy Ann
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-09-894-998-35
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US-09-894-998-35/c
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Matches 144;
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RESULT 14
US-10-023-529-50/c
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Best Local Simi
Matches 232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 582 AGGIGGGGAGGCGGATGAGGGGTGGGGGACCCCTTGACGTCACCAGAAGGAG-GTGCCGG 640
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND IREALING TITLE OF INVENTION: ATHEROSCLEROSIS FILE REPERENCE: 10797-004001.
CURRENT APPLICATION NUMBER: US/10/023,523
CURRENT FILING DATE: 2001-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                583
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 1614;
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Pred. No. 0.21;
0, Mismatches 230; Indels
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Patent No. US20020147140a1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
                                                                       PRIOR PELICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR PELICATION NUMBER: US 09/517,849
PRIOR PILING DATE: 1090-03-02
PRIOR PILING DATE: 1997-11-26
PRIOR PELICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1997-06-03
SUMMBER OF SEO ID NOS: 53
NUMBER OF SEO ID NOS: 53
LENGTHARE: FESTERQ for Windows Version 4.0
LENGTH: 1614
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Best Local Similarity 46.9%;
Matches 206; Conservative
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US-10-023-523-45
                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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US-09-764-877-2718
                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
                                                                                                                                                                                                                                                                                             TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Lees, Robert S.
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Arjona, Anibal A.
IIILE OF INVENTION: NOVEL LOW DENSITY LIPOPROIEIN BINDING
IIILE OF INVENTION: ATHERORICAL SAND THEIR USE IN DIAGNOSING AND TREATING
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-0
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-11-27
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2718
                                                                                                                                                                                    DB 10; Length 9968;
                                                                                                                                                                            4.8%; Score 45; DB 10; I
llarity 45.8%; Pred. No. 0.27;
Conservative 0; Mismatches 270;
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                                                                                              ) IYPE: DNA
) ORGANISM: Homo sapiens
US-09-764-877-2718
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 50
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TITLE OF INVENTION: MOVEL LOW DENSITY LIEOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
FITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3381 GCGCGGCGCCGCCGCCCACGGCCCGCCCCCCCCGCGGGGCCCCGGCTGCGCG
                                                                                                                                                                                   DB 12; Length 12425;
                                                                                                                                                                                   Score 45, DB 12, Length 12,
Pred. No. 0.28,
0; Mismatches 230; Indels
                                  NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 50
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PRIOR FILING DATE: 2000-07-14
PRIOR PARIOR ELING DATE: 2000-07-14
PRIOR PARIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031, 930
PRIOR PILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
PRIOR APPLICATION NUMBER: US 60/048,547 PRIOR FILING DATE: 1997-06-03
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Matches 206; Conservative
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Law, Simon W.
                                                                                                                           ORGANISM: Homo sapiens
US-10-023-529-50
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APPLICANT: Lees, Ann M.
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RS-10-023-523-50/c
                                                                                           LENGTH: 12425
                                                                                                            TYPE: DNA
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                                                                           DB 12; Length 12425;
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                                                                                          Pred. No. 0.28;
0; Mismatches 230;
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                                                                           Score 45;
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                                                                        Query Match 4.8%;
Best Local Similarity 46.9%;
Matches 206; Conservative
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              ; TYPE: DNA; ORGANISM: Homo sapiens US-10-023-523-50
LENGIH: 12425
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through 1195 correspond to -1155 through -1 from
Figure 2."
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APPLICANT: Worlshita, Kaoru
TILE OF INVENTION: No. 5916763el Promoter for VEGF Receptor VIMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 941; DB 2; I
100.0%; Pred. No. 1.6e-191;
iive 0; Mismatches 0;
               US-08-920-8286.13
US-08-920-8286.13
US-08-844-196-11
US-08-945-988-7
US-09-949-155-49
US-08-949-155-49
US-08-949-155-49
US-08-949-155-49
US-08-919-964-49
US-08-919-968-10
US-08-913-24
US-08-913-24
US-08-913-0118-4
US-08-913-0118-4
US-09-343-0118-4
US-09-343-0118-4
US-08-343-0118-4
US-08-343-0118-4
US-08-757-6648-16
US-08-757-6648-16
US-08-757-6648-16
   US-08-362-577C-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATIORNEY/AGENI INFORMATION:
NAME: Dow, Katen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-063500US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1167843-9600
TELEFAX: 415-543-9600
                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                      US-08-556-424-1
Sequence 1, Application US/08556424
Patent No. 5916763
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1745 base pairs IYPE: nucleic acid
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Best Local Similarity 100.
Matches 941; Conservative
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CITY: San Francisco
STATE: California
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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   FILING DATE:
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                                                                                                                                                                                               941
1 GCCGAAAAAGACACGGACAC......GCCGGGTCTTTGGCCGCGGG 941
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Sequence 49,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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Compugen Ltd.
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US-08-232-463-14
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US-08-984-709A-49
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US-08-483-533-36
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US-09-017-631-23
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US-08-921-177-13
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US-08-786-164-5
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              GenCore version
Copyright (c) 1993 - 2002
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Maximum Match 1008
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length: 2000000000
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6245512el Promoter for VEGF Receptor
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APPLICATION DATA:

RILING DATE:

CLASSTORM COMBER: US/NG COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMPANS COMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPAX: 415-543-5043
                                                                                                     STREET: One Market Flaza,
CIIY: San Francisco
STAIE: Callfornia
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LCCATION: 1.1195
TITLE OF INVENTION: NO. NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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FEATURE:
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/note= "Nucleotides numbered 1
through 1195 correspond to -1195 through -1 from
Figure 2."
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100.0%; Score 941; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1.6e-151;
Matches 941; Conservative 6; Mismatches 6;
Townsend and Crew
                Steuart Tower,
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Sequence 1, Application US/09263914 Patent No. 6245512

US-09-263-914-1

GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Morishita, Kaoru

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750 TCGGGTGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATTACCCGGGGAAGTGGTTGTCTC 849
                                                                                                                                                                                                                                                                                                                                                 730 GCGGACACICCICTCGGCTCCICCCGGCAGCGGCGGCGGCTCGGAGCGGGCTCCGGGGC 789
                                                                                                                                                                                                                                                                    Length 2313;
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Sequence 1, Application US/09427353
Fatent No. 6375959;
GAPELICANT: THOMAS, KENNETH A.
APPLICANT: GOLDMAN, COREY K.
APPLICANT: BETT, RICHARD L.
APPLICANT: BETT, ANDREW R.
ITILE OF INVENTION: GENE THERAPY FOR INHIBITION OF TILLE OF INVENTION: ANGIOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: J. MARK HAND - MERCK 5 CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
                                                                                                                                                                   Score 194.8; DB 1;
Pred. No. 3.7e-33;
0; Mismatches 2;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,353
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                                                                                                                                                               Guery Match 20.7%;
Best Local Similarity 98.1%;
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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                         LENGTH: 2313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TYPE: nucleic acid
          SEQUENCE CHARACTERISTICS:
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TELEX:
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CORRESPONDENCE ADDRESS:
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                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-232-538-5
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ZIP: 07065-0907
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: NJ
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                                                                                                                                      1040 CCGTAGCCGCAGGGAAGCGAGGCTGGGAGGAAGAAGAGGTGAGGTGGGGAGGGGGATGAG 1059
                                                                                                                                                                                                                                                                                                   1180 CTCCGGGGCTCGGGTGCAGCGGCCAGCGGCGCCTGGCGGGGGGGAGATACCCGGGGAAGT 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1340 GGTTGTCTCCTGGCTGGAGCCGCGAGACGGCGCTCAGGCGCGGGGGCCGGCGGCGGGGGA 1359
                                                                                                                   AGCACCTCCCCACGCGCGCCCCGGGCCACCCGCCCTCGTCGGCCCCCGCCCTCT 540
                                                                                                                                                                                                     600
                                                                                                                                                                                                                                                                                    999
860 GGGTGGAGGAGTCTGCAAGGATTTCCTGAGCGCGATGGGCAGGAGGAGGGGCAAGGGCA 519
                                                          920 AGAGGGCGCGGAGCAAAGACCCTGAACCTGCCGGGGCCCGCTCCCGGGCCCGGGTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1220 GCGCCCAGGCGGACACTCTCTCGGCTCCTCCCGGCAGGGGCGGCGGCGGCGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781 CTCCGGGGCTCGGGTGCAGCGGCCCCTGGCGGCGAGGATTACCCGGGGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              841 GGTTGTCTCCTGGCTGGAGCCGCGAGCGGCGCTCAGGGCGCGGGGCGGCGGCGGCGA
                                     421 AGAGGGCGCGGAGCAAAGACCCTGAACCTGCCGGGCCGCGCGCTCCCGGGCCCGCGTCGCC
                                                                                                                                                                                                541 CCGTAGCCGCAGGGAAGCGAGCCTGGGAGGAGAAGAGGGGTAGGTGGGGAGGCGATGAG
                                                                                                                                                                                                                                                                              601 GGGTGGGGGACCCCTTGACGTCACCAGAAGGAGGTGCCGGGGTAGGAAGTGGGCTGGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Thomas, Kenneth A.
APPLICANT: Kendall, Richard L.
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1400 ACGAGAGGACGGACTCTGGCCGCCGGGTTTGGCCCCCGGG 1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000 126 E Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W.III
REGISTRATION NUMBER: 35,403
REFERENCY/DOCKET NUMBER: 18881A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/232,538
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-232-538-5

; Sequence 5, Application US/08232538

; Patent No. 5712380

; GENERAL INFORMATION:
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ZIP: 07065-0907
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STREET: F.C.
TWY: Rahway
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CURRENT APPLICATION NUMBER: US/09/051,363
FILING DATE: 07-APR-1998
FILING DATE: 07-APR-1998
FILING DATE: 07-APR-1996
FILING DATE: 07-CT-1996
APPLICATION NUMBER: B/211892 JP
FILING DATE: 23-JUL-1996
APPLICATION NUMBER: 7/296476 JP
FILING DATE: 07-CT-1996
APPLICATION NUMBER: 7/296476 JP
FILING DATE: 07-CT-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                20.7%; Score 194.8; DB 4; 98.1%; Pred. No. 3.7e-33; live 0; Mismatches 2
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TITLE OF INVENTION: VEGE-BINDING POLYPEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    910 cGGACTCTGGCGGCCGGGTCTTTGGCCGCGGG 941
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REFERENCE/DOCKEY NUMBER: 06501/012001
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-051-363-1; Sequence 1, Application US/09051363; Patent No. 6270993
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APPLICANT: Shibuya, Masabumi
APPLICANT: Okamoto, Masaji
APPLICANT: Niwa, Mikio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Matsumoto, Tomoe APPLICANT: ASANO, Makoto
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COMPUTER: IBM Compatible
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MEDIUM TYPE: Diskett
STRANDEDNESS: single
                TOPOLOGY: linear NOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                              HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
CRIGINAL SOURCE:
US-05-427-353-1
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790 TCGGGTGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATTACCCGGGGAAGTGGTTGTCTC 849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       850 CTGGCTGGAGCCGCGAGACGGGCGCTCAGGGCGCGGGGGCGGCGGCGGCGAACGAGGA 909
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2523;
                                                                                                                                                                                                                                                                                                                                                        Indels
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APPLICANT: KENDALL, RICHARD L
TILLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL
MUMBER OF INVENTION: CELL GROWTH FACTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                               Score 194.8; DB 4;
Pred. No. 3.7e-33;
0; Mismatches 2;
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SIREET: P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 CGGACTCTGGCGGCCGGGTCGTTGCCCGGGG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  910 CGGACTCTGGCGGCCGGGTCTTTGGCCGCGGG 941
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,164
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION WIMBER: 36,545
REFERENCE/DOCKET NUMBER: 16866
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-4720
TELEPX: 908-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08786164
Patent No. 5861484
                                                                                                                                                                                       CELL TYPE: placental tissue
                                                                                                                                                                                                                              NAME/KEY: Coding Sequence
LOCATION: 250...2523
                                                                                                                                                                                                                                                                                                               20.7%;
ilarity 98.1%;
Conservative
INFCRMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AITORNEY/AGENT INFORMATION:
                                       LENGIH: 2523 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIATE: No
SIATE: No
COUNTRY: USA
TO: 07065-0900
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                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                  TOPOLOGY: line
MOLECULE TYPE: c
ORIGINAL SOURCE:
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TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
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                   single
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SIRANDEDNESS: SI
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                                                                S.
                                                                                                  IMMEDIATE SOURCE:
                                            MOLECULE TYPE:
HYPOIHETICAL: N
ANTI-SENSE: NO
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                                                                                                                                                                US-08-785-420-1
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                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                     61 TCGGGTGCAGCGCCAGCGG--GCCTGGCGGCGAGGATTACCCGGGGAAGTGGTTGTCTC 118
                                                                                                                                                                                                                                                                                                                                                                                       730 GCGGACACTCCTCGGCTCCTCCCCGGCAGCGGCGGCGGCTCGGAGCGGGCTCCGGGGC 789
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                  1 GCGGACACTCCTCGGCTCCTCCCCGGCGCGGGGGGGGGCTCGGAGGGGGCTCCGGGGC 60
                                                                                                                                                                  Length 2651;
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MacLennah, David H
APPLICANT: O'BILEN, Peter J.
TITLE OF INVENTION: DIAGNOSIS FOR PORCINE MALIGNANT
TITLE OF INVENTION: HYPERTHERMIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                           Ouery Match
20.7%; Score 194.8; DB 2;
Best Local Similarity 98.1%; Pred. No. 3.8e-33;
Matches 208; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Bell, Seltzer, Park & Gibson
P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 CGGACTCTGGCGGCCGGGTCGTTGGCCGGGGG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                     910 CGGACTCTGGCGGCCGGGTCTTTGGCCGCGGG 941
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No. 6001976th Carolina 28234
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APPLICATION NUMBER: US 08/030,159
FILING DATE: 15-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/785,420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08785420 Patent No. 6001976
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Layton, Jr., Samuel G. REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 704-377-1561
        INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 2651 base pairs TYPE: nucleic acid strandedness: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: 15378 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 704-334-2014
TELEX: 57-5102
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS
                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-786-164-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-785-420-1
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Db 12932 CTGAGGGCGCGGAGGGCGCGGTGGGGCCCGAGGCCGCGGCGGGACCGCGGCGGCCGG 12991
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                                                                                                                                                                                                                                                                                                                                   563 CIGGGAGGAAGAAGAGGTAGGTGGGGAGGCGGATGAGGGGTGGGGGACCCCTTGACGTC 622
                                                                                                                                                                                                                                                                                                                                                                                                                                      623 ACCAGAAGGAGGIGCCGGGGIAGGAAGIGGGCIGGGGAAAGGIIATAAAICGCCCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              743 TCGGCTCCTCCCCGGCAGCGGCGGCTCGGAGCGGGCTCCGGGGTCGGGTGCAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NAKAMURA, TAKESHI
TILLE OF INVENTION: NOVEL BRAIN-SPECIFIC ADAPTER MOLECULE GENE
TILLE OF INVENTION: THEREOF, AND ANTIBODY THERETO
                                                                                                                                                                                                                            Score 55.4; DB 3; Length 15378;
Pred. No. 0.0017;
0; Mismatches 166; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IRM PC PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: PILLSBURY, MADISON & SUTRO, L.L.P. STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 7898/225948 FLECOMMUNICATION INFORMATION:
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FILING DATE: 11-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENI INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08729416C Patent No. 6013767 GENERAL INFORMATION:
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DNA (genomic)
                                                                                                                                                                                                                               5.58;
48.38;
                                                                                               CLONE: Porcine RYR1 Gene POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                              674 3CCCCCCCCCCTCGCCTCTTCATCGAGGTCCGCGGAGGCTCGGAGCGCCCAGGCGG 733
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                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                   Query Mauch 5.7%; Score 53.2; DB 3; Length 1785; Best Local Similarity 51.7%; Pred. No. 0.0041; Matches 121; Conservative 0; Mismatches 113; Indels 0
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COMPUTER VISA
CONFUTER TEADABLE FORM:
MEDIUM TYPE; Floppy disk
COMFUTER: TEAPPY disk
COMFUTER: TEM PC. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTIWARE: PATENT RPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FLING DATE:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08232463
Patent NJ. 5670367
GENERAL INFORMER, F.
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. 6
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAMS: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 INAU
TELECHMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                 TYPE: nucleic acid
STRANDEDNESS: double strand
TOPJUGY: linear
INFORMATION FOR SEQ ID NO: 16. SEQUENCE CHARACTERISTICS: LENGTH: 1785 base pairs
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                    ; MOLECULE TYPE: CDNA to mRNA US-08-729-416C-16
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GENERAL INFORMATION:
APPLICAN: Kieff, Elliott D.
APPLICAN: Kieff, Elliott D.
APPLICAN: Ballesas, Mary E.
IIILE OF INVENTION: VREUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
TILLE OF INVENTION: VREUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
CURRENT APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
SAPLICA E SEQ ID NOS: 3
SOFTWARE: PALENT WERE PALENT WERE PALENT WERE PALENT WERE PALENT WERE PALENT WERE PALENT WERE TO NOS: 3
LENGTH. 801
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                                                                                                                                                                                                                                                                                                                                                                                                                                  466 GGAGGGCAAGGGCAAAGGCGCGGAGCAAAAAACCCCTGAACCTGCCGGGGCCGCGCTCC 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          586 GGGGAGGCGGAIGAGGGGTGGGGGACCCCTTGACGTCACCAGAAGGAGGTGCCGGGGTAG 645
                                                                                                                                                                                                                                                                          346 ASAGCIGAGIAAGCCGGGIGGAGGGAGICIGCAAGGAITICCIGAGGGGAIGGGCAAGA 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                      Length 7218;
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                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1091 RERREREREREREREREREREREREATCGCAAGCICCCTCGAC 1049
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                                                                                                                                                                Query Match 5.5%; Score 51.4; DB 1; L Best Local Similarity 3.8%; Pred. No. 0.011; Matches 13; Conservative 197; Mismatches 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09298568 Patent No. 6322792
STRANDEDNESS: single JORCLOGY: linear
                                                                                ) CLONE: pTZgpt-Fls
US-08+232-463-14
                               IOPOLOGY: line
IMMEDIATE SOURCE:
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US-09-298-568-3/c
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602 CGIGGAGGIGGGICIGGAGGASCGGCGGGCAAGGGGCGCGGCCGACGACGAGG 661
                                       763 GOGGGGGCTCGGAGCGGGCTCCGGGGTGCAGCGGCCAGCGGGCGCCTGGCGGCG 822
482 GOCGCCGGCAGCGGCGGGCGCGGCCAGCGGGGCAGCACCCGGGGCGCCCCCTGCGGGCG 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666 IATAAATCGCCCCCGCCCTCGGCTGCTCTTCAICGAGGTCCGCGGGGGGCTCGGAGCGGG 725
                                                                 823 AGGATTACCCGGGGAAGTGGTIGTCTCCTGGCTGGAGCCGCGAGACGGGCGCTCAGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(625..637, 1201..1346, 1605..1651, 2303..2482,
2617..2772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(625..637, 1201..1346, 1605..1691, 2303..2482,
2617..2772)
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Delcuve, Genevieve APPLICANT: Awang, Gregor IIILE OF INVENTION: Recombinant DNA Molecules and Expression TIILE OF INVENTION: Vectors for Itssue Plasminogen Activator
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                                                                                                                                                                                           883 UGGGGCCGCGCGCGCGAACGAGGACGGACTCTGGCGGCCG 925
                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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27-JUN-1997
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US-08-683-795A-33/C
Sequence 33, Application US/08883795A
Patent No. 5985607
GENERAL INFORMATION:
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CLASSIFICATION: 4.2
AITOKNEY/AGENT INFORMATION:
WAWE: Gravelle, Micheline
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 46,261
REFERENCE/DOCKEI NUMBER: 76
FELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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EDNESS: single
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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FILING DATE: 27-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 122; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s: Ontario
RY: Canada
MSH 3Y2
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LOCATION:
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FEATURE:
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                                                                                                                                                                                     818 CGCCGAGGATTACCCGG-GGAAGTGGTTGTCTCCTGGCTGGAGCCGCGAGACGGGGCTC 876
                 398 GGGCAGGAGGAGGGCCAAGGGCCAAGAGGCCCGGAGCAAAGACCTGAACCTGCCGGGC 457
                                                                                                                                                                                                                                         578 GGGTAGGTGGGGAGGCGGATGAGGGGTGGGGGACCCCTTGACGTCACCAGAAGGAGGTGC 637
                                                                                                                                                                                                                                                                                                                   698 TCGAGGTCCGCGGGAGGCTCGGAGCGCGACACACACTCCTCGGCTCCTCCCCGG 757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: TOMLINSON, James
APPLICANT: COT Therapeutics, Inc.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
TITLE OF INVENTION: CYCLASE
                                                   518 CCCTCGTCGCCCCCCCCCCCTCCGTAGCCGCAGGAAGCGAGCCTGGCAGGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    758 CAGCGGCGGCGCTCGGAGCGGCTCCGGGGCTCGGGTGCAGCGGCCAGCGGCCCTGC
                                                                                       0;
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Pred. No. 0.042;
0; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 44481-5027-01-US
CURRENT APPLICATION NUMBER: US/09/473,716
CURRENT FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: PCT/US/98/13540
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/070,901
PRIOR FILING DATE: 1997-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: human type V adenylyl cyclase
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Patent No. 6436672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 CGGTGTGGGGGGCCCGGGCGCG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.2%;
Best Local Similarity 51.1%;
Matches 114; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1997-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 08
PRIOR FILING DATE: 1997-07-0
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PALENTIN VEr. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (139)...(3921)
US-09-473-716-1
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SEQ ID NO 1
LENGTH: 4523
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US-09-473-716-1
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417 GGCAAGAGGGGGGGAGCAAAGACCCTGAACCTGCCGGGGCCGCGCTCCCGGGCCCGCGT 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 AGCCGGCTGSAGGGAGTCTGCAAGGATTTCCTGAGGGGGATGGGCAGGAGGAGGAGGAAG 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      687 CGCGGGGGTCGCGGGGTCGCGGGGTCGCGGGGGTCGCGGGGGTCGCGGGGGTCGCGGG 628
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                  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell
SIREPT: Two First National Plaza Suite 2100
SITY: Chicago
                                                                                                                                                                               MEDIUM IYPE: Floppy disk
COMPUTER: IBA PC COMPATIble
DERAITMG SYSTEM: PC-LOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                  27373/8235
                                                                                                                                                                                                                                                                                  PCI/US91/06532
                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 27:
TALECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
                                                                                                                                                                                                                                                                                                                                                                                30,060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1335 base pairs
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        CURRENT APPLICATION DAIA:
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Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                               NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                           312/984-9740
    CORRESPONDENCE ADDRESS:
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                    Illinois
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CLASSIFICATION:
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                                                                                                                                       644 TACTCACCGIGCACCCCCATCTCCGCGCCTGGCCGGGGTCCCTCAGGGACCTGGGGCGCG 585
                                                            786 GGGCTCGGGTGCAGCGGCCCAGCGGCCCTGGCGGCGAGGATTACCCGGGGAAGTGGTTG 845
                                                                                                                                                                                                846 TCTCCTGGCTGGAGCCGCGAGACGGCCCTCAGGGCGCGGGCCGGCGGCGGGGGGAACGAG 905
                                                                                                                                                                                                                           APPLICANT: Sytkowski, Arthur J.

IITLE OF INVENTION: Production and Use of Recombinant
TITLE OF INVENTION: Protein Multimers With Altered Biological Activity
FILE REPRENCE: B1497-05A
CURRENT APPLICATION NUMBER: US/09/018,138
CURRENT FILING DATE: 1998-02-03
EARLIER APPLICATION NUMBER: 08/890,929
EARLIER PILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastsEEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666 TATAAATCGCCCCCCCCCCTCGCTGCTCTATCGAGGTCCGCGGGAGGCTCGGAGCGCG 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      726 CCAGGCGGACACTCCTCTCGGCTCCTCCCGGCAGCGGCGGCGGCTCGGAGCGGGCTCCG 785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Herpes Simplex Viruses
Vaccines and Methods
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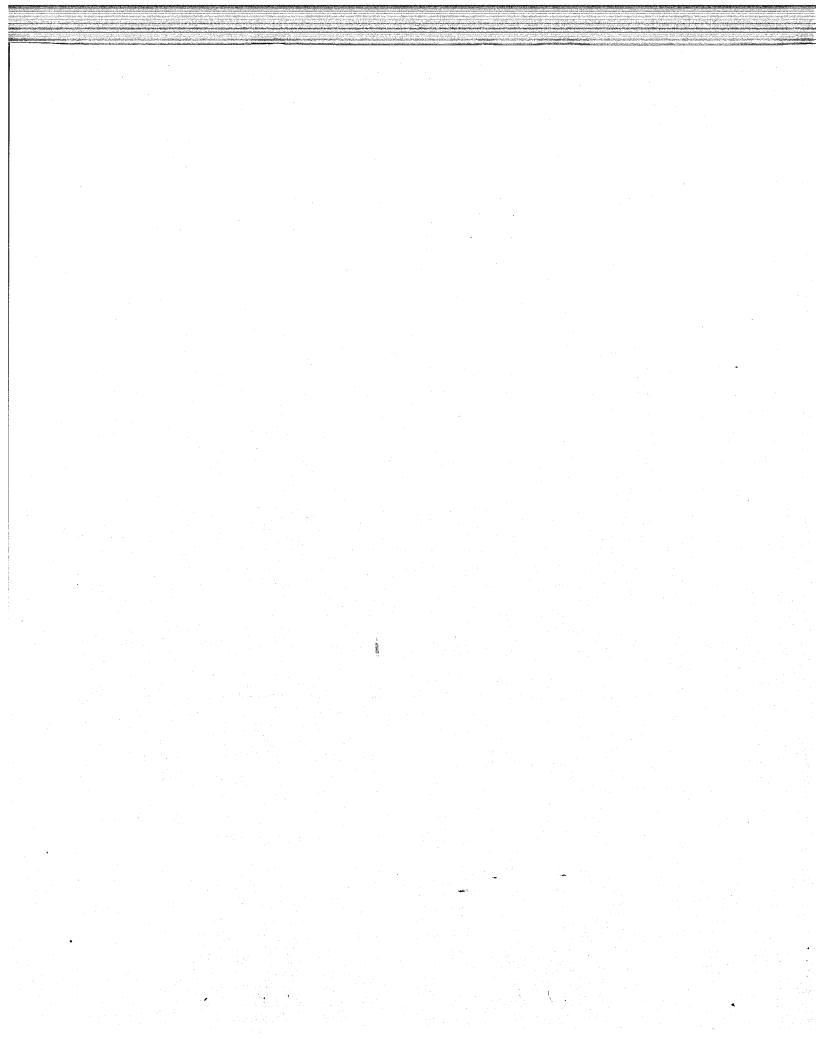
@CI-US91-0632-1/C
| Sequence | Application Pc/TUS9106532
| Sequence | Application Pc/TUS9106532
| APPLICANT: Rolzman, Bernard
| TITLE OF INVENTION: Recombinant Herr
| TITLE OF INVENTION: Vaccines and Men NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                            09-018-138-1/c dependention US/09018138 dependent 1, Application US/09018138 Patent No. 6187564 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                           906 AGGAC 910
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Pred. No. 0.085;
0; Mismatches 133; Indels 0
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
897 GCGAACG----AGAGGACGGACTCTGGCGGCCCGGGTCTTTGGCCGCGG 940
                    Silet, Constitute of Indee, Kazushi Bodner, Sarah M.
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New Jersey
COUNTRY: USA
COMPUTE: ROBOIL
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IND PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
RECISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5804
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/280,590A
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                %3.09-280-590a-36
; Sequence 36, Application US/09280590a
; Patent No. 6303772
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 29-Mar-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 5703 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                 APPLICANT: Hirai, Hiroshi
Sherr, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.0%;
Best Local Similarity 48.8%;
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
                                                                                                   RESULT 15
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Human colon cancer Human colon cancer

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Oligonucleotide Oligonucleotide

Human colon cancer

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Kaposi's sarcoma-a Lung cancer relate Lung cancer relate

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Rhadino virus cis-Gene #3953 used to

SVEGF-RI gene. Ho Human soluble vasc

DNA encoding novel Flt-lextraFAStm/cy

cDNA encoding amin

Soluble VEGF recep Human VEGF recepto

soluble VEGF

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/note- "E26 transformation specific sequence"
1068..1071
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/note="E26 transformation specific sequence"
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/note= "(Claim 4)"
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Chemically treated
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.
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                         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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AAS61170
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ABQ67063
AAS46352
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misc\_feature

Result Q ö

from the mammal, selecting cells which have incorporated and express the gene and reimplanting them into the mammal (claimed). The transgenic or chimeric animal can be used as a disease model, or as a bioreactor for the production of large amounts of protein.

Sequence 1745 BP; 315 A; 501 C; 621 G; 308 I; 0 other;

or artisense kNa, which reduces vascular permeability or has artimitogenic activity, operably liked to the VECF receptor promoter, it can be used to inhibit tumour anglogenesis following its introduction into the endothelial cells links the tumour, or control anglogenesis in a mammal by transfecting cells explanted

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/note= "forms separated palindrome with bases 1109-
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/note= "forms separated palindrome with bases 1698-
1103"
                                                                                       cAMP response element binding protein/activated transcription factor"
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/note- "E26 transformation specific sequence"
1157..1160
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/note- "transcription arrest site"
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note= "exon 1"
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/note= "E26 t
1164..1171
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                                                            ACCGICGCGGAGGCGCGGGCTTCCCTTGGATCGGACTTTCCGCCCCTAGGGCCAGGC 300
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                                                1 GOOGAAAAAGACACGGACACGCTCCCTGGGACCTGAGCTGGTTCGCAGTCTTCCCAAAG 60
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Score 941; DB 18; Length 1745;
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al Similarity 100.0%;
941; Conservative 0
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This purified nucleic acid comprises the vascular endothelial growth factor (VEGF) receptor Fit-1 gene promoter region. The sequence was determined from 3 overlapping clones isolated from a human placental genomic library using a human Fit-15 cDNA fragment as probe. Also claimed are: an expression vector comprising the nucleic acid molecule; a host cell transformed with the vector; and a transgence or climeric animal containing the vector. The promoter can be used to provide endothelial cell specific gene expression, and control angiogenesis. e.g. inhibition of tumour angiogenesis. The host cell or a be used to screen for compounds that regulare the activity of a VEGF receptor promoter or modulate VEGF receptor transcription or that are (ant)agonists of the VEGFVEGF receptor regulatory system (claimed). The vector can be used to treat diseases affecting the vascular endothelium, e.g. hypertension, thrombosis, atherosclerosis, restenosis, inflammatory diseases, hemosphilia, wound healing, diabetic retinopathy. Theumatoid arthritis and blood cell traficking. When it further comprises a gene encoding a protein, polypeptide, hormone, ribozyme

Vascular endothelial growth factor receptor promoter · usefui to develop products to treat, e.g. tumours, hypertension, thrombosis, atherosclerosis or inflammatory diseases

WPI; 1997-280976/25.

Claim 4; Fig 2A-B; 70pp; English.

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/clone_lib="LTI_TRE006_PL2"
/tissue_type="placenta"
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/note="wetcrir: pCWNSPORT 6; Site_1: Not1: 1st strand cDNA
was primed with a Not1-oligo(d1) primer. Five prime end
enriched, double-stranded cDNA was digested with Not 1 and
cloned into the Not 1 and Eco RV sites of the pcWNSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email::fliang@lifetech.com URL.:
http://fulllength.invitrogen.com"
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11. (bases 1 to 1002)
11. W.B., Gruber, C., Jessee, J. and Polayes, D.
11. W.B., Gruber, C., Jessee, J. and Polayes, D.
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Contact; Genoscope
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/clone="CSODI033YD17"
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TITLE
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/cloned into the NotI-oligo(dT) primer. Five prime end enriched, double-stranded CDNA was digested with Not I and Coned into the NotI and Eoc RV sites of the pCWYSPORI 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies.
// Contact: Feng Liang Life Technologies.
// Contact: Feng Liang Life Technologies.
// Rockville, Maryland 20850, USA Fax: (1) 301 510 8371
// Email: fliang@lifetech.com URL:
// Contact: A contact of the Contact Dive
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                            Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqreffgenoscope.cns.fr. Web : www.genoscope.cns.fr.
Location/Qualifiers
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ALS51816
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1025)
                                                                                                                                                                                                                                  Email: genomicsfhri.co.jp

HRI buman cDNA project: 5'- & 3'-end one pass sequencing: Helix

Research Institute: oDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

Location/Qualifiers
                                     Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Rawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         781 CICCGGGGCICGGGIGCAGCGGCCAGCGGCGCCIGGCGAGGAIIACCCGGGGAAGI 840
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Location/Qualiflers
Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.
1 (bases 1 to 652)
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Live 0; Mismatches 5; Indels 0
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                                                                                                                                                                                1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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/clone_lib=PLACEI'
/lissue_type="placenta"
/note="vector: pMR188FL3"
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/db_xref="taxon:9506"
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                                                                                          HRI human cDNA project
                                                                                                           Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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Fax: 81-438-52-3986
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Best Local Similarity 97.77
Matches 216; Conservative
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/note="vector: provided in the strand country is strand country was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the poWNSPORI 6 vector. Library was normalized Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 510 8371 Email: filliang Mifetech.com URL.

Example: Alliang Mifetech.com URL.

Example: Alliang Mifetech.com IRL.

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Manmalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
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22.6%; Score 212.2; DB 9;
Best Local Similarity 97.8%; Pred, No. 4.3e-31;
Matches 222; Conservative 3; Mismatches 1;
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/tissue_type="placenta"
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/tissue_type="placenta"
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Euvaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Eutharia: Primates: Catarrhini; Hominidae: Homo.
Manmalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.
I (bases 1 to 584)
S. Helton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lenhskha, I., Scearce, M., Brescelli, J., Gradoni, G., Cilfton, S.,
Hillier, L., Marra, M., Pape, D., Willie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
M., Gibbons, M., McCann, R., Cole, R., Isagareishvili, R., Williams, I.,
Endocrine Pancreas Consortium
Uppublished (2000)
Coher_Esis: iklado, xlaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Endocrine Pancreas Consortium
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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                                                                  1k.4a07.y1 HR85 islet Homo sapiens CDNA clone IMAGE: 5780553 5
similar to TR:012954 012954 SOLUBLE VASCULAR ENDOTHELIAL CELL
GROWTH FACTOR RECEPTOR. ;, mRNA sequence.
                               790 TEGGGTGCAGCGGCCAGCGGCGCCTGGCGGCGAGGATTACCCGGGGAAGTGGTTGTCTC
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High quality sequence stop: 476.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
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/tissue_type="placenta"
/tis
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Romo.
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                            http://fulllength.invitrogen.com"
175 c 202 g 108 t
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                                                                                                                                                   DB 9:
Email : fliang@lifetech.com URL
                                                                                                                                                   Score 211.4; DB 9;
Pred. No. 6.2e-31;
0; Mismatches 1;
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/clone="CS0D1030xL03"
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/note-"Organ Pancreas; Vector: pBluescript SK(-); Site_1:
Noti Site_2: Xho; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Ilouis, MO 5310, E-mail: hinoue@imgate.wustl.edu, Tel:
114-382-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 206.6; DB 14; Length 584; Pred. No. 5.2e-30;
/clone_lib="HR85 islet"
/tissue_type="Purified pancreatic islet"
/lab_host="DH108"
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Answer vector provided to site_1: Not1; 1st strand convariant which a Not1-oligo(dT) primer. Five prime end enriched, double-stranded convariant site of the prime end convection of the provided site of the provided site of the provided site of the provided by Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies. Sockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: flangfalfetech.com URL: http://fullength.invlirogen.com"
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1. (bases 1 to 740)
Li,W.B.; Gruber,C., Jessee,J. and Polayes,D.
Full-length.cDNA libraries and normalization
Unpublished (2001)
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121 STIGICICCISSCISSASCCSCSAGACGSSCSCICASGSCSCSGSGCCGGCGCCGCCGAA 180
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BP 191 91006 EVRI cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/db_xref="taxon:9606"
/clone="CS0D1051Fp21"
/clone_11b="LT_LNEL006_PL2"
/tissue_type="placenta"
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//issue_type="placenta"
//note="Vector: pCWVSPORT 6; Site_l: Not!: lst strand cDNA
was primed with a Not!-oligo(d1) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
life Technologies. Context: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                            729 GGCGGAGACICCTCICGGCTCCTCCCCGGCAGCGGCGCCGCTCGGAGCGGGCTCCGGGG 788
                                                                                                                                 848
                                                                                                                                                         61 CTCGGGTGCAGCGGCCAGCGGGCGCTGGCGGGGATTACCCGGGGAAGTGGTTTTT 120
                                                                                                                                                                                                                         849 CCTGGCTGGAGCCGCCAGACGGGCGCTCAGGGCGCGGGGGCGGCGGCGGCGGCGAACGAGAGG 908
                                                                                                                                                                                                                                                                      121 CCIGGCIGGAGCCGCGAGACGGGCGCICAGGGCGCGGGGCCGGCGGCGGCGGCGAACGAGAGG 180
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    Gaps
                                                                                       1 GGCGGACACTCCTCTCGGCTCCTCTTGCACCGGCGGCGGCTCGGAGCGGGCTCCGGGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers
                                                                                                                                    CICGGGIGCAGCGGCCAGCGGGCGCCTGGCGGCGAGGAITACCCGGGGAAGIGGIIGICI
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  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
267 c 272 g 209 t
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BP 191 91005 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                   181 ACGACICTGGCGCCGGGCGTTGGCCGCGGG 213
  Mismatches
                                                                                                                                                                                                                                                                                                              909 ACGGACICIGGCGGCCGGGTCTTIGGCCGCGGG 941
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/db_xref="taxon:9606"
/clone="CSODI006YF20"
  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prime, mRNA sequence.
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Best Local Similarity
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  209;
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DEFINITION
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ORIGIN
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TITLE
JOURNAL
    Matches
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pcMvSPORI 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville / Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com*
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: placenta: Vector: pcMvSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSPORT 6 vector. Library was constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 867)
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BP 191 91005 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
_Location/Qualifiers
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Pred. No. 3.9e-29; 
1; Mismatches 1; Indels
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                                                                                                                                                              Li.W.B., Gruber C., Jessee, J. and Polayes, D. Utll-length CDNA libraries and normalization Unpublished (2011)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                     AL540382.1 GI:12870475
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Best Local Similarity 98.2%;
Matches 224; Conservative
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                                                                                    Homo sapiens
                                                                 human.
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ORIGIN
                   VERSION
KEYWORDS
SOURCE
CRGANISM
                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
                                                                                                                                             REFERENCE
AUTHORS
ACCESSION
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Search completed: December 8, 2002, 12:49:39
Job time: 1237.21 secs

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3395 CCCGACTCCCTTGAAGTGGATGGACCCCGGAAACCATTTTGACAGAGTATACACAATC 3454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 74.6; DB 1; Length 5406;
Pred. No. 4.1e-14;
0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA: 1992
APPLICATION NUMBE: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Imclone Systems Incorporated STREET: 180 Variok Street
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PRIJA APPLICATION DATA: APPLICATION LAFA: APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
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FILING DATE: 19521119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/07977451 Patent No. 5270458 GENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: LE
IELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
IELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.88;
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                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 5406 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SIngle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89; Conservative
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208..4308
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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STATE: New York
COUNTRY: U.S.A.
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Best Local Similarity
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US-07-813-593-3
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US-07-977-451-5
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Pred. No. 1.1e-14;
0; Mismatches 23; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lemischka, Ihor R. TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
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CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/07/813,593
FILING DATE: 19920415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
                                  APPLICATION NUMBER: US/07/930,548A FILING DATE: 23-NOV-1992 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: NEW YORK
COUNTRY: U.S.A.
2IP: 10014
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/728,513
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                        31,298-01
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793, 065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/07813593 Patent No. 5185438 GENERAL INFORMATION:
                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 31,2:
TELECOMMUNICATION INFORMATION:
TELEPRONE: 201-831-3344
TELEFAX: 201-831-336
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         30,637
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Best Local Similarity 79.6%;
Matches 90; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4236 base pairs
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             CURRENT APPLICATION DATA:
                                                                                                                                                                              NAME: Gordon, Alan M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..4068
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US-07-930-548A-7
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3355 CCCGACICCCTITGAAGIGGAIGGCCCGGAAACCAITITITGACAGAGIAIACACAAITC 3454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.8%; Score 74.6; DB 1; Length 5406; 78.8%; Pred. No. 4.1e-14; Live 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08252517
Patent No. 5548065
GENERAL INFORMATION:
APPLICANT: Lemischka, Thor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL.
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inclone Systems Incorporated
SIRRET: 180 Varick Street
CITY: New York
              COUNCEL SEPLICATION NUMBER:
CLASSIFICATION NUMBER:
CLASSIFICATION: 336
PRIOR APPLICATION: 336
FRING APPLICATION: 336
FRING DAIE: 24-DEC.1951
PRIOR APPLICATION NUMBER: 05/07/93,065
FILING DAIE: 14-NOV-1991
PAPOR APPLICATION NUMBER: 05/07/28,913
FILING DAIE: 15-NOV-1991
PAPOR APPLICATION DAIA:
FILING DAIE: 28-JUN-1991
PRIOR APPLICATION NUMBER: 05/07/728,913
FILING DAIE: 28-JUN-1991
PRIOR APPLICATION NUMBER: 05/07/728,913
FILING DAIE: 28-JUN-1991
PRIOR APPLICATION NUMBER: 05/07/728,913
FILING DAIE: 28-JUN-1991
PRIOR APPLICATION NUMBER: 05/07/728,913
FILING DAIE: 28-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEM-3-PPP
                                                                                                                                                                                                                                                                                                                                                                                                NAME: Felt, Irving N.
AEGISTRATION NUMBER: 28,601
REPERNCE/DOCKET NUMBER: LEM-
IELECOMMUNICATION INFORMATION:
IELEPHONE: 212-645-1405
IELEFRAX: 212-645-2054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGIH: 5406 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 78.8 Matches 89; Conservative
    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208..4311
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; LOCATION:
US-07-946-507-3
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NAME/KEY:
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FEATURE:
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US-08-252-517-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.8%; Score 74.6; DB 1; Length 5406; 78.8%; Pred. No. 4.1e-14; Live 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIFOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-U01-1991
RICHAR APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 212-645-1405
APPLICATION NUMBER: US 07/813,593 FILING DATE: 24-DEC-1991 PRIOR APPLICATION DATA:
                                                                       US 07/793,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-946-507-3; Sequence 3, Application US/07946507; Patent No. 5283354
                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5406 base pairs
                                                                                           15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 5406 base pairs
NUCLEIC ACID
DEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: N-terminal
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208..264
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265..4308
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CORRESPONDENCE ADDRESS:
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                                                                         APPLICATION NUMBER:
FILING DATE: 15-NOV
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MOLECULE TYPE: CDNP
HYPOTHETICAL: NO
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Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEW YORK
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LOCATION:
FEATURE:
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LOCATION:
FEATURE:
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US-07-977-451-5
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Sequence 5, Application US/07506397A
Pater. No. 5621090
GENERAL INDEMATION:
APPLICANT: Lemischka, Ihor R.
THILE OF INVENTION: TOTIPOTENT HEMAIOPOIETIC SIEM CELL
THILE OF INVENTION: EMEDPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,397A
FILLING DATE: 19220666
CLASSIFICATION: 536
PHIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FROR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                   CCREES ON THE STATE OF THE STREET INCORPORATED SIREET: 180 VARICK SIREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REJISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-PPPPPP IELECOMMUNICATION INPORMATION:
IELEPHONE: 212-645-1405
IELEPAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/675,666
FILING DATE: 02-APR-1991
ALTERNYAGENI INFORMATION:
NEWEL: FEIL, ITVING N.
REDISTRATION NUMBER: 28,601
                                                                                                                                                                                                                                                                                     ZIP: 10014
CCAPUIER READABLE FORM:
MEDIUM IYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SIRANDEDNESS: single
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                                                                                                                                                                                                                                                  NEW YORK
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ANTI-SENSE: 'N
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; LCCAIION:
US-07-906-397A-5
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Pred. No. 4.1e-14;
0; Mismatches 24; Indels 0
                                                        PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 07/977,451
FILING DATE: 19 NOV-1992
PRIOR APPLICATION DATE:
APPLICATION DATE: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 15-APP-1992
PRIOR APPLICATION DATA:
APPLICATION DATE: US PCT/US92/02750
FILING DATE: 02-APP-1992
PRIOR APPLICATION DATA:
APPLICATION DATE: US PCT/US92/02750
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION DATA: US O7/93,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: US 07/679,666
FILING DATE: US 07/679,666
FILING DATE: US 07/679,666
FILING DATE: US 07/679,666
FILING DATE: US 07/679,666
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    APPLICATION NUMBER: US/08/252,517
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                  FILING DATE: 31-0CT-1994
CLASSIFICATION: 530
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAGMENT TYPE: N-terminal
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Best Local Similarity 78.84
Matches 89; Conservative
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208..264
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265..4308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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; LOCATION:
US-08-252-517-5
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NAME/KEY:
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FEATURE:
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                                                                                                          3395 CCCGACTCCCTTTGAAGTGGATGCCCCCGGAAACCATTTTTGACAGAGIATACACAATTC 3454
                                                                                  69 CICGACTICCTCTGAAATGGATGGCTCCTGAATCTATGTTGACAAAAICTACAGCACCA 128
                                                                                                                                                                                         3455 AGAGGATGTGTGGTCTTTCGGTGTGTGCTCTGGGAAATATTTCCTTAGGT 3507
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                                                                                                                                                                 129 AGAGGGACGIGIGGICTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
24.8%; Score 74.6; DB 1; Length 5406; 78.8%; Pred. No. 4.1e-14;
                                             24; Indels
                                             0; Mismatches
                                             Conservative
  Query Match
Best Local Similarity
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                                             Matches
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3455 AGAGCGATGTGTGTCTTTCGGTGTTGCTCTGGGAAATATTTCCTTAGGT 3507

129 AGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181

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3395 CCCGACTCCCTITGAASIGGATGGCCCGGAAACCATTITGGACAGAGTAAACACAATIC 3454
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                                                                                                                                                                                                                                                                                                                                                                 3455 AGAGCGAIGTGIGGGCCTTTCGGTGTGTGCTCTGGGAAATAIITCCTIAGGT 3507
                                                                                                                                                                                                                                                                                                                                           129 AGAGCGACGTGTGTTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                          24.8%; Score 74.6; DB 1; Length 5406; 78.8%; Pred. No. 4.1e-14; tive 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-05-021-324-5
US-05-021-324-5
Sequence 5, Application US/09021324
Fatent No. 5912133
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TILLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC SIEM CELL
TILLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC SIEM CELL
TILLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC SIEM CELL
TILLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC SIEM CELL
TILLE OF INVENTION: TOTIPOTENT LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCLO. Systems Incorporated
STREET: IRG. Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATE: TW 81102961
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,513
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
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FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
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CLASSFEICATION:
PRIOR APPLICATION DAIA:
APPLICATION NUMBER: US/07/977,451
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        us/09/021,32
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                        Conservative
mat_peptide
265.:4308
                                                                   sig_peptide
208..264
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                                                                                                                                                               Query Match
Best Local Similarity
Matches 89; Conserv
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NAME/KEY:
LOCATION:
FEATURE:
                                                                      NAME/KEY:
                                                                                           LOCATION:
                                                                                                                 US-08-601-891-5
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                                                                                                                                  TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: InClone Systems incorporated STREET: 180 Varick Street CITY: New York
                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,891
FILING DATE: 15-FEB-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIORA APPLICATION DATA.

PRIORA APPLICATION NUMBER: US 07/977,451

FILING DATE: 19-NOV-1992

PRIOR APPLICATION NUMBER: US 07/906,397

FILING DATE: 26-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US PCT/US92/05401

FILING DATE: 26-JUN-1952

PRIOR APPLICATION DATA:

APPLICATION NUMBER: TW 81102561

FILING DATE: 15-APR-1992

FRICK DATE: 15-APR-1992

FRICK DATE: 15-APR-1992
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FILING DATE: 02-APR-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/670 600
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APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEM-3-7P
                                                     ; Sequence 5, Application US/08601891; Patent No. 5747651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Feit, Irving N. REGISTRATION NUMBER: 28,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: LEI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
                                                                                                   GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 5406 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212-645-2054
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                                                                                                                                                                                                                                                                                                                                                  ZIP: 10014
COMPUTER READABLE FORM:
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LOCATION: 208..4311
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                         New York
U.S.A.
                                                                                                                                                                                                                                                                                                                                 COUNTRY:
              RESULT 10
US-08-601-891-5
                                                                                                                                                                                                                                                                                                            STATE:
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3355 CCCGACICCCTITGAAGIGGAIGGCCCGGGAAACCAITITTGACAGAGTAACACAATC 3454
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                                                                                                                                                                                                                                                                                                                                                                                                                                             24.8%; Score 74.6; DB 5; Length 5406; 78.8%; Pred. No. 4.1e-14; Live 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.8%; Score 74.6; DB 5; Length 5406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application PC/TUS9205401
GENERAL INFORMATION:
APPLICANT: Lemischka, Thor R.
TITLE OF INVENTION: TOITPOPENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.

ZIP: 10014
COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPATARE: Perentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/U5401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
SIREET: 140 VARICK SIREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEM-3-PPPPT
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ALIGNERY/AGENT INFORMATION:
RAKE: FELL, INVING N.
REGISTRAIL'M NUMBER: 28,601
REFERENCE/COCKET NUMBER: LEM-
IELECOMMUNICATION INFORMATION:
IELEPHOME: 212-645-105
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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LENGTH: 5406 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                      Conservative
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208..4308
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208..4308
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STRANDEDNESS: single
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208..4311
                                                               IOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
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Matches 897 Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: NEW YORK STATE: NEW YORK COUNTRY: U.S.A.
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CLASSIFICATION:
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LCCATION:
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FEATURE:
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; LOCATION:
PCT:-US92-05401-5
                                                                                                                                                                                           NAME/KEY:
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                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 CTCGACTTCCTCTGAAATGGATGGCTCCTGAATCTATCTTTGACAAAATCTACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3455 AGAGCGATGTGTGTGTTCGGTGTGTGTCTCTGGGAAATATTTCCTTAGGT 3507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 AGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 24.8%; Score 74.6; DB 2; Length 5406; Best Local Similarity 78.8%; Pred. No. 4.1e-14; Matches 89; Conservative 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LEMISCHKA, IHOR R.
TITLE OF INVENTION: Totipotent Hematopoietic Stem Cell
TITLE OF INVENTION: Receptors And Their Ligands
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02750
FILIG DATE: 1920402
CLASSIFICATION: 435
ATTORNEY/AGGNT INFORMATION:
NAME: FEIT, IRVING N
REGISTRATION NUMBER: 28,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: LEM-3-PPPPT TELECOMMUNICATION INFORMATION: TELEPHONE: 212-645-1405 TELEFAX: 212-645-2054 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                         REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application PC/TUS9202750 GENERAL INFORMATION:
      NAME: Feit, Irving N. REGISTRATION NUMBER: 28,601
                                                                                                                         INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
ELENGTH: 5406 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
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208..264
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265..4308
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208..4311
                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
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LOCATION:
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US-09-021-324-5
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PCI-US92-02750-7
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3473 CCCGACICCCTTIGAAGIGGATGGCCCCGGAAACCAITTIGACAGAGTAIACACAATC 3532
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                                                                                                                                                                                                                         APPLICANI: Millauer, Birgit
APPLICANI: Gazit, Aviv
APPLICANI: Gazit, Aviv
APPLICANI: Levitzki, Aviv
TILLE OF INVENTION: Fik-1 is A Receptor For Vascular
TILLE OF INVENTION: Endothelial Growth Factor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: December 8, 2002, 07:52:31
                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds
SIREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30,742
---- 7683-060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/193,829
FILING DATE: 09-FEB-1994
ATIONESY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/443,861
FILING DATE: 22-MAY-1995
                                                                                                                   ; Sequence 1, Application US/08443861
; Patent No. 5851999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: COTUZZÍ, LAURA A.
RECISTRAITON NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 76
IELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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(212)869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5470 base pairs
                                                                                                                                                                                     Ullrich, Axel
Risau, Werner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                            New York
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MOLECULE TYPE:
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US-08-443-861-1
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APPLICANT:
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                                                                                   3395 CCCGACTCCCTTTGAAGTGGATGGCCCGGAAACCATTTTTGACAGAGTATACACAAIIC 3454
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                                                           69 CTCGACTTCCTCTGAAATGGATGGCTCCTGAATCTATCTTTGACAAAATCTACAGCACCA 128
                       Gabs
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                                                                                                                                          129 AGAGGGACGTGTGGTCTTACGGAGTATTGCTGGGGAAATCTTCTCCTTAGGT 181
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                     Indels
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TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWANE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19921116
  Pred, No. 4.1e-14;
0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEM-3-7PT
                                                                                                                                                                                                                                                                               Sequence 5, Application PC/TUS9209893 GENERAL INFORMATION:
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NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEPHONE: 212-645-1405
TELEPHONE: 212-645-1405
SEQUENCE CHARACIERISTICS:
Best Local Similarity 78.8%;
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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208..264
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265..4308
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
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COMPUTER READABLE FORM:
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208..4311
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Best Local Similarity
Matches 89; Conserve
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: U.S.A.
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LOCATION:
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FEATURE:
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Gaps

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Human receptor typ
pTK gene LpTK25.
Protein tyrosine-k
Human FlK2/flt3 ty
Human STK-1 CDNA.
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                                                                                                                                                                                                                                                      Flk2 receptor prot
Human flk-2 cDNA.
                                                                                                                                                                                                                                                                           Murine foetal live
Human flk-2 recept
Human flk-2 cDNA.
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Nucleotide sequenc
                                                                                                                                                                                                                                                                                                                                               FLT4 receptor tyro
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Murine foetal live
Murine flk-1 cDNA.
flk-1 cDNA sequenc
                                             Human flk-1 coding
Murine flk-1 cDNA.
                                                                    Flk1 receptor prot
                                                                                           Murine flk-1 recep
Sequence of murine
                                                                                                                                        Human receptor typ
                                                                                                                                                                                                                                                                                                                                    Human Flt4/VEGFR-3
                                                                                                                  Human receptor typ
                                                                                                                             Human receptor typ
                                  Murine flk-1 cDNA.
Human flk-1 coding
                                                                                  Mouse flk-1
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Human
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AAA37815
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AAT03090
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AAQ49756
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AAX77515
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AAQ40916
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                                                                                                      AAQ64049
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                                                                                                                                                                                                                                                                                                             ABL91753
                        AAQ29957
  AAT38735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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  (first entry)
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4111
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  (without alignments)
2048.198 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                         / SIDS2/gogdata/geneseq/geneseqn-embl/NA1981.DAT:*
/ SIDS2/gogdata/geneseq/geneseqn-embl/NA1981.DAT:*
/ SIDS2/gogdata/geneseq/geneseqn-embl/NA1982.DAT:*
/ SIDS2/gogdata/geneseq/geneseqn-embl/NA1984.DAT:*
/ SIDS2/gogdata/geneseq/geneseqn-embl/NA1985.DAT:*
/ SIDS2/gogdata/geneseq/geneseqn-embl/NA1985.DAT:*
/ SIDS2/gogdata/geneseq/geneseqn-embl/NA1987.DAT:*
/ SIDS2/gogdata/geneseq/geneseqn-embl/NA1988.DAT:*
/ SIDS2/gogdata/geneseq/geneseqn-embl/NA1988.DAT:*
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                                                                                                                                                                                                                                  4370478
               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                  tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                          2185239 seqs, 1125999159 residues
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                                                                                                                              US-09-778-900A-3_COPY_200_500
                                                                                                                                                                                                                                                                                         Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                           IDENTITY_NUC Gapext 1.0
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Maximum DB seq length: 200000000
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Match
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                                                                                                                                 Title:
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flk-2 coding flk-2 cDNA.

polynucleoti Flt4/VEGFR-3

/standard\_name= "Single nucleotide polymorphism (SNP)"

/\*tag= c replace (454, A) /\*tag= d

variation

intron exor

Human flt-1 gene D Human polynucleoti

AAD19454 ABL91752 AAS70286 ABL91751

Description

ΩI

Length DB

Score 301

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/\*tag=

EP11:0123-A2

05-SEP-2001

Human polynucleoti Human VEGFR-2 enco Human KDR genomic

AAQ28272 AAV99829 ABL91754 AAF83308 AAV34763

726 4017 7680 4044 4071 4071 4071 4225

100.0 38.0 37.5 25.3 25.3 25.3 25.3 25.3 25.3

1114.4 1112.8 76.2 76.2 76.2 76.2 76.2

A novel type III R Human receptor tyr DNA encoding novel Human polynucleoti

Ω

/\*tag= b 279..726 278

STK-1 cDNA.

CDNA.

Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; Plasmodium; virus; /iroid; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.

Human polynucleotide SEQ ID NO 95.

(first entry)

28-MAY-2002

ABL91752;

Вb

ABL91752 standard; NA; 4017

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The invention relates to novel sequence and polymorphisms in the human flr-1 gene. Fit-1 is one of the two receptors for vascular endothelial growth factor (VEGFR-1). The invention also relates to a method for diagnosing one or more single uncleotide polymorphism (SNP) in human flr-1 gene. The method is useful for assessing the predisposition and/or susceptibility of an individual to diseases mediated by an flr-1 ligand, to recognise individuals who are particularly at risk from developing these conditions, and in the development of new drug therapies that selectively target one or more allelial variants of the fit-1 gene. Flt-1 polymorphisms are used in the diagnosis and treatment of cancer and angiogenic diseases such as diabetic retinopathies, psoriasis, rheumatoid angiogenic diseases such as diabetic retinopathies, osed in mapping the chuman genome and to elucidate the genetic component of the diseases, as contain a trial risk and endometricals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful as components in databases useful in sequence identity, genome mapping, pharmacogenetics and other search analyses. The flt-1 antagonist is useful in the preparation of a medicament for treating VEGF-mediated diseases in a human diagnosed as having a single nucleotide polymorphism at one or more of the defined positions. The present sequence is human flt-1 gene DNA fragment related to the invention. This DNA fragment
                                                                                                                                                                                                                                                                                                                                                                          Diagnosing single nucleotide polymorphism in human flt-1 gene, for assessing predisposition or susceptibility to diseases mediated by an flt-1 ligand, comprises determining the nucleic acid sequence at one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AATGTCCTTTGGTTGGACAGCCTTTAGATTAGAACCTACTGTAACAAAAAAACTCTTAAAG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contains exon 24 and adjacent intron sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 23; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0%; Primatches 301; Conservative 0;
20-FEB-2001; 2001EP-0301489.
                                                                               24-FEB-2000; 2000GB-0004232.
                                                                                                                                                           (ASTR ) ASTRAZENECA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              more point positions
                                                                                                                                                                                                                                                                                                           WPI; 2001-608199/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 T 301
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                                                                                                                                                                                                                                   Smith JC;
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Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired

Rost S, Hadwiger P;

Kreutzer R, Limmer S, (RIBO-) RIBOPHARMA AG

WPI; 2002-270454/32

terminal bases

09-JAN-2001; 2001DE-1000586. 09-JAM-2001; 2001DE-1000586

DE10100586-C1 Home sapiens

11-APR-2002.

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The invention relates to a method for inhibiting expression of a target gene (ABL51658-ABL5177) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential uncleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known or oligonucleotides, probably because the unpaired overhand increases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AGACTCGACTICCTUTGAAAIGGATGGCTCCTGAATCTATCITIGACAAAAICTACAGCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 24; Length 4017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4017 BP; 1236 A; 915 C; 903 G; 963 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel human diagnostic protein #6090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.0%; Score 114.4; DB 2.99.1%; Pred. No. 2.5e-26; iive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stability and thus intracellular concentration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 68-69; 104pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS70286 standard; cDNA; 7680 BP.
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Best Local Similarity 99.1
Matches 115; Conservative
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RESULT 2 ABL91752

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The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL51797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides
                                                              Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; Plasmodium; virus; virold; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, Id developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3194 CICSCCICCCITIGAAAIGGATGGCCCCAGAAACAATTTTTGACAGGIGIACACAAICC 3253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 CTCGACTTCCTCTGAATGGATGGCTCCTGAATCTATCTTTGACAAAAICTACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor tyrosine kinase; vascular endothelial cell growth factors; cancer; tumour; diagnosing; monitoring; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 AGACCGACGICTGGCTCTTACGGAGTATTGCTGGGGAAATCTICTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence: 4044 BP; 1163 A; 885 C; 1021 G; 975 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 76.2; DB 24;
Pred. No. 5e-14;
0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stability and thus intracellular concentration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hadwiger P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A novel type III RIK gene - the KDR gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Page 67-68; 104pp; German.
          Human polynucleotide SEQ ID NO 94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ28272 standard; cDNA; 4071 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rost S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.3%;
79.6%;
                                                                                                                                                                                                                                                                                                                             09-JAN-2001; 2001DE-1000586.
                                                                                                                                                                                                                                                                                                                                                                              09-JAN-2001; 2001DE-1000586.
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Best Local Similarity 79.65
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Limmer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-270454/32
                                                                                                                                                                                                                                                                                                                                                                                                                               (RIBO-) RIBOPHARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        terminal bases
                                                                                                                                                                                                                            DE10100586-C1.
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                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                          11-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kreutzer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ28272;
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AAQ28272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (11). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1 is useful in gene therapy techniques (11). (11) is useful for generating antibodies against It, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostics, forensics, gene mapping, identification of mutations responsible for generic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 CCAAGAGCGACGŢGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 112.8; DB 23
Pred. No. 1.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 6090; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.5%;
98.3%;
                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                     2000US-0540217.
2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT, Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; ABG06099
                                                                                                                                                  W0200175067-A2
                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                        31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                   23-AUG-2000;
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ABL91751;

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RESULT 4 ABL91751

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Length 4044;

Key

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This nucleotide sequence encodes a novel receptor tyrosine kinase, termed KDR (see AAM80997), that is expressed on human endothelial cells. KDR is activated by vascular endothelial growth factor and mediates a mitogenic signal. It is implicated in clinical necangiogenesis. KDR CDNA was isolated from a human umbilical vein endothelial cell lambda phage cDNA library using a 576-bp DNA probe that had been generated by PCR (see also AAV99850-53). The predicted protein product has amino acid differences from the previously protein product has amino acid differences from the previously protein product has amino acid differences from the previously contains ATV (44) to Arg), 835 (Asn to Lys), 848 (Glu to Val) and 1347 (Thr to Ser), producing a protein predicted by computer modeling to have higher activity and functionality. The invention also relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3154 CTGGCCTCCTTTGAAATGGATGGCCCAGAAACAATTTTTGACACAGTGTACACAATCC 3253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment encoding human KDR, a DNA fragment encoding the intracellular portion of KDR with or without a membrane anchor sequence, purified forms of associated human KDR, and human mutant forms of KDR. KDR, fusion proteins or fragments can be used in assays to identify antagonists and agonists of human KDR (claimed). Antagonists of KDR useful for treating diseases involving neoangiogenesis e.g. diabetic retinal vascularization, cancers (e.g. brain, breast, etc.) and forms of inflammation e.g. rheumatoid artirits, psoriasis, contact dermatitis and hypersensitivity reactions. The polynucleotides are useful to screen for KDR reactions.
                                                                                                                                                                                                                                                                                                                                                                    Human receptor tyrosine kinase protein, KDR - useful e.g. to screen for antagonists useful to treat diseases involving neoangiogenesis e.g. diabetic retinal vascularization, cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antayonists/agonists and for gene therapy (e.g. by introducing a gene portion encoding a KDR protein containing functional ligand binding and membrane anchoring moieties but not tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3254 AGAGIGACGICIGGICIIIIGGIGITIIGCIGIGGGAAAAIIIIICCIIAGGI 3306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       They are also useful to measure levels of human KDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4071 BP; 1169 A; 894 C; 1027 G; 981 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 76.2; DB 20;
Pred. No. 5e-14;
0; Mismatches 23;
                                                                                                                                                                                                                             Thomas KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polynucleotide SEQ ID NO 97.
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                                                                                                                                                                                                                             Tebben A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1a; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.68;
                                                        98WO-US12569
                                                                                                           97US-0050962
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                                                                                                                                                                       MERI ) MERCK & CO INC
                                                                                                                                                                                                                             Mão X,
                                                                                                                                                                                                                                                                                      1999-095333/08.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW80997
                                                        17-JUN-1558;
                                                                                                           18-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 - MAY - 2002
                                                                                                                                                                                                                             Kendall RL,
23-DEC-1998.
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                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       즵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a novel type III receptor tyrosine kinase was been. A labelled ENCRY-BamHI DNA Segment derived from clone BTII1081.8 was used as a probe to rescreen a human endothelial cDNA library (#L10246) for 5'full length DNA segments of the gene from which the insert portion of BTII1081.8 is derived. A synthetic probe designed from nucleotides 3297-335 of BTII1081.8 is then used to isolate more 3' full length clones. One of the clones, designated BTIII200.2 is cloned into paluescript Ks and the synthetic oligonucleotide ICGAOCCCGC ATG GAG cloned, which esynthetic oligonucleotide CGAOCCCGC ATG GAG cloned, which esynthetic oligonucleotide ICGAOCCCGC ATG GAG cloned, which esynthetic oligonucleotide Glu, the first two amino acids encoded by the KDR gene, forming BTIIV140, which is then purified on a CScI density gradient. This was sequenced, together with BTIII081.8, and BTIII129.5 to comprise the entire ORP of 4,068 nucleotides of the KDR gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3194 CTGCCTCCCTTTGAAATGGATGGCCCAGAAACAATTTTTGACAGAGTGTACACAATCC 3253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 CICGACITCCTCTGAAATGGATGGCTCCTGAATCTATCTTTGACAAAATCTACAGGACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitogen; necangiogenesis; angiogenesis; diabetic retinopathy;
breast cancer; brain cancer; inflammation; rheumatoid arthritis;
psoriasis; contact dermatitis; hypersensitivity; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3254. AGAGTGACGTCTGTTTTGGTGTTTTGCTGTGGGAAATATTTTCCTTAGGT 3306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 76.2; DB 13; Length 4071;
Pred. No. 5e-14;
); Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 AGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding type III receptor tyrosine kinase - useful for diagnosing the onset of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDR; receptor tyrosine kinase; human; signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4071 BP; 1172 A; 894 C; 1024 G; 981 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human receptor tyrosine kinase KDR cDNA.
  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV99829 standard; cDNA; 4071 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 7; 101pp; English.
                                                                                                                                                                                                                                                                                                                                            (AMCY ) AMERICAN CYANAMID CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.3%;
                                                                                                                                                                                                                                                                                      91US-0657236.
                                                                                                                                                                                                                          92WO-US01300.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match $ 25.3°
Best Local Similarity 79.6°
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Terman BI;
                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-316117/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR26999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09858053-A1
                                                                                                                                                                                                                             20-FEB-1992;
                                                                                                                                                                                                                                                                                      22-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                     Carrion ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-APR-1999
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AAV99829;

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AAV99829

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Length 4071; indels

11-APR-2002

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/*tsg* b
/note= "extracellular domain coding fragment (AAF83310)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to determining whether a compound is capable of binding to a receptor protein complex comprising a vascular endothelial growth factor receptor? (VEGFR-2) receptor protein and a neuropilin-1 (NP-1) receptor protein. One method comprises introducing a sample comprising the compound to the receptor protein and allowing the compound to bind to the complex. Signaling through VEGFR-2 is enhanced in the presence of the NP-1 co-receptor. The methods of the invention can be used for identifying novel pro- and anti-anglogenic compounds. The present sequence represents the DNA encoding a human VEGFR-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3263 CTCGCCTCCCTTTGAAATGGATGGCCCCAGAAACAATTTTTGACAGAGTGTACACAATCC 3322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 CICGACTICCICTGAAAIGGAIGGCICCTGAAICTAICTIIGACAAAAICTACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinase insert domain containing receptor; KDR; screening; inhibitor; vascular endothelia! growth factor; VEGF; angiogenesis; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "kinase insert domain containing receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining compounds which bind to a complex comprising vascular endothelial growth factor receptor-2 and Neuropilin-1 to provide superior pro- and anti-anglogenic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3323 AGAGTGACGTCTGTTTTGGTGTTTTGCTGTGGGAAATATTTTCCTTAGGT 3375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 AGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4225 BP; 1204 A; 940 C; 1067 G; 1014 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 76.2; DB 22
Pred. No. 5.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Limberg BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 32-39; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
/*tag= a
/product= "VEGFR-2"
71..2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= KDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV34763 standard; DNA; 4236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.3%;
79.6%;
                                                                                                                                                                                                                                26-OCT-2000; 2000NC-US29579.
                                                                                                                                                                                                                                                                                                                                                                     Rosenbaum JS, Whitsker GB,
                                                                                                                                                                                                                                                                                                                       (PROC ) PROCIER & GAMBLE CO
                                                                                                                                                                                                                                                                            99US-0162367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 79.6
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human KDR genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-308686/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAB62475
                                                                                                                                    WC200131346-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                             misc_feature
                                                                                                                                                                                                                                                                            28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1958
                                                                                                                                                                                  03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV34763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV34763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XXX
XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for inhibiting expression of a target capene (ABL91658-ABL91797) in a cell by introducing at least one coligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides coligoribonucleotides for attiesense inhibition of gene expression useful coligoribonucleotides for attiesense inhibition of gene expression useful coligoribonucleotides present in pathogens (e.g. Plasmodium or viruses/virolds, pathogenic on humans, animals or plasmodium or viruses/virolds, pathogenic on humans, animals or plants) or against effective inhibition of gene expression than use of known coligonucleotides, probably because the unpaired overhang increases catability and thus intracellular concentration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3194 CTGGCCTCCCTTTGAAATGGATGGCCCAGAAACAATTTTTGACAGAGTGTACACAATCC 3253
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 CTCGACTTCCTCTGAAATGGATGGCTCCTGAATCTATCTTTGACAAAATCTACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor protein; vascular endothelial growth factor receptor-2; VEGFR-2; neuropilin-1; NP-1; co-receptor; human; anglogenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3254 AGAGTGACGTCTGGTCTTTGGTGTTTTGCTGGGGAAATATTTCCTTAGGT 3306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 76.2; DB 24; Length 4071;
Pred. No. 5e-14;
0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 AGAGCGACGTGTGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4071 BP; 1169 A; 894 C; 1025 G; 983 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                     Hadwiger P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Page 71-72; 104pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
70..4140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                       Rost S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF83308 standard; DNA; 4225
                                                                                                                                                                                                                                09-JAN-2001; 2001DE-1000586.
                                                                                                                                                                                                                                                                            09-JAN-2001; 2001DE-1000586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human VEGFR-2 encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    il Similarity 79.6
90; Conservative
                                                                                                                                                                                                                                                                                                                                                                       Limmer S,
                                                                                                                                                                                                                                                                                                                            (RIBO-) RIBOPHARMA AG.
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-270454/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            terminal bases
                                                                                                                                       DE10100586-C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       Kreutzer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-2001
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RESULT 8 AAF83308 Key

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3355 CCCGACTCCCTITGAAGTGGATGGATGGCCCCGGAAACCATTITGACAGAGTAIACACAATTC 3454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes murine foetal liver kinase 1 (flk-1), a protein tyrosine kinase. Isolated antibodies, pref. monoclonal, raised against the extracellular portion of flk-1 can be used to assay for ilk receptors on the surface of haematopoletic stem cells, and to isolate positive cells. The antibodies can also be used as, or to octain ligands, which stimulate the proliferation and/or differentiation of stem cells. The ligands can be used, e.g. for treating anaemia, or bone marrow damage resulting from cancer
                                                                                                                                                                                                                                                                                                                                                           Anti-foetal liver kinase 2 (fik-2) antibodies - useful in assays, for isolating haematopoietic stem cells expressing receptor and for obtaining ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine; flk-2; flk-1; cell isolation; fetal liver kinase; receptor; monoclonal; polyclonal; antibody; tyrosine kinase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.8%; Score 74.6; DB 17; Length 5404; 78.8%; Pred. No. 1.8e-13; ive 0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 AGAGCGACGIGIGICITACGGAGTATIGCIGIGGGAAAICTICICCITAGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5404 BP; 1411 A; 1297 C; 1423 G; 1273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Columns 51-62; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
208..4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a /product= "flk-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX77516 standard; cDNA; 5404 BP.
                                                      9105-0679666.
9105-0728913.
9105-0793065.
9105-0813593.
9205-0906397.
9205-0975049.
9405-055269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemotherapy, or radiation.
9108-0579666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89; Conservative
                                                                                                                                                                                                                                   NOTABLE DAIN PRINCETON
                                                                                                                                                                                                                                                                                                         WPI; 1996-392678/39.
P:PSDB; AAT38735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine flk-1 cDNA
                                                                                                                                                                                                                                                                       Lemischka IR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5912133-A.
    02-APR-1991;
                                                                                                                                                                                              31-0CT-1994;
                                                                                                                                                        12-NOV-1992
                                                                                -JUN-1991
                                                                                                15-NOV-1991
                                                                                                                                      26-JUN-1592
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                                                                                                                                                                                                                                                                                                                                                                                                   This sequence encodes a novel human growth factor receptor, kinase insert domain containing receptor or KDR. This receptor is capable of binding to the vascular endothelial cell growth factor, VEGF and its used in a screening assay which identifies compounds that inhibit VEGF action on KDR. Such compounds which inhibit binding of VEGF to the KDR may inhibit anglogenesis and thus be useful for treating caneer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1194 CICGCCTCCCTTTGAAATGGATGGCCCCAGAAACAATTTTTGACAGAGTGTACACAATCC 3253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 CTCGACTTCCTCTGAAATGGATGGCTCCTGAATCTATTTTGACAAAATCTACAGCACCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                             Screening assay for vascular endothelial cell growth factor antagonists - using recombinant cells expressing receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3254 AGAGTGACGTCTGTTGCTGTTTGCTGTGCGGAAATATTTTCCTTAGGT 3306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine; foetal liver kinase 1; flk-1; protein tyrosine kinase; monoclonal; antibody; extracellular domain; receptor assay; haematopoletic stem cell; ligand; stimulation; proliferation; differentiation; treatment; anaemia; bone marrow damage; cancer chemotherapy; radiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 AGAGCGACGTGTGGTCTTACGGAGTATTGCTGTGGGAAATCTTCTCCTTAGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.3%; Score 76.2; DB 19; Length 4236; 79.6%; Pred. No. 5.1e-14; Ive 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4236 BP; 1216 A; 938 C; 1062 G; 1020 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 7A-M; 51pp; English.
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                                                                                                                                                                                (AMCY ) AMERICAN CYANAMID CO.
                                                                                                                      92US-0930548.
                                                                                                                                            97US-0810116.
                                                                                  97US-0810116.
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90; Conservative
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Query Match Best Local

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                                                                                                                                                                                                                                                                                               2430 IGGCTGIGCAAGAGGGGAGAGGCTGTTCATAATAGAAGGTGCCCAGGAAAAGAAGACTT 2489
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                                                                                     IGCCAGCAASIGGGAGIIIGCCCGGGAGACIIAAACIGGGCAAAICACTIGGAAGAGG-857
                                                                                                                                                                                                                                                                                                                                                621 GGAGCIGAICACICIAACAIGCACCIGTGIGGCIGCGACICTCTTCTGGCTCCTAITAAC 680
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                              2190 GCGCATGGCACCCATGATCACCGGAAATCTGGAGAATCAGACAACAACATTGGCGAGAC
                                                                                                                                      441 CAACCACAAAATACAACAAGAGCCTGGAATTATTTTAGGACCAGGAAGCAGCACGCTGTT
TCAGGAAGCACCATACCTCCTGCGAAACCTCAGTGATCACACAGTGGCCATCAGCAGTTC
                                                                 CACCACITIAGACIGICAIGCIAAIGGIGICCCCGAGCCICAGAICACIIGGIIIAAAAA
                                                                                                                                                                                                           501 TATTGAAAGAGCCACAGAAGAGGATGAGGTGTCTATCACTGCAAAGCCCACCAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2070 CATCTTGATTGTGGCATTTCAGAATGCCTCTGCAGGACCAAGGCGACTATGTTTGCTC 2129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 AGCCAGGAAIGTATACACAGGGGAAGAAATCCICCAGAAGAAAGAAATTACAAICAGAGA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine flk-2 receptor protein tyrosine kinase - used to stimulate proliferation and/or stimulation of primitive mammalian haematopoietic stem cells in vitro or in vivo.
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                                                                                                                                                                                                                 retal liver kinase-1; flk-1; protein tyrosine-kinase receptor; hematopoiesis; stem cell; ds.
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     3687 CCTCCTGCAAGCAATGCGCAGCAGGATGGCAAAGACTATAT 3728
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65.0%; Pred. No. 1.3e-204;
tive 0; Mismatches 576; 1
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92US-0906397.
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                                                                                         AAQ79070 standard; cDNA;
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28-JUN-1991;
15-NOV-1991;
24-DEC-1991;
26-JUN-1992;
12-NOV-1992;
30-APR-1993;
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                                                                                                                                                                                             Mouse flk-1
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Search completed: December 8, 2002, 09:38:18 Job time: 518.686 secs

December 8, 2002, 07:52:47; Search time 2363.64 Seconds (Without alignments) 11586.276 Willion cell updates/sec D64015\_COPY\_500\_1440 941 1 GCCGABABAGACACGGACAC.......GCCGGGTCTTTGGCCGCGGG 941 4109280 GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd. 2054640 segs, 14551402878 residues tal number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 em\_htg\_hum:\*
em\_htg\_inv:\*
em\_htg\_other:\*
em\_htg\_aus:\* Minimum DB seq length: 0 Maximum DB seq length: 2000000000 em\_fun:\*
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em\_in:\* em\_ro:\* em\_sts:\* em\_un:\* em\_om:\*
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AX478548 Sequence AC128409 Rattus no AC12229 Mus muscu AJ224863 Mus muscu BD003577 Gene ther 182801 Sequence 5 ARIGISAGO SEQUENCE E13256 Human mRNA PRO30842 SEQUENCE F14000 Human solub AX51602 Human fil m AX060540 SEQUENCE AC130633 Rattus no AC129765 Rattus no AC125560 Rattus no AC125580 Rattus no AC125580 Rattus no AC125580 Rattus no AC125580 Rattus no AC125739 Rattus no AC12739 Rattus no AC127739 Rattus no AR157385 Sequence D64016 Human gene AL139005 Human DNA Sequence Sequence E10168 Promoter of AX251105 Sequence Sequence Sequence Sequence Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description AX458547 S AX251106 S AX348648 AX344257 SUMMARIES AC122299 MMU224863 AX458548 AC128409 AC119074 E14000 AR030842 HUMES AL139005 E10168 AX251105 AX251868 AX344256 AX348647 AR163540 AX060540 AC129765 AR157385 182801 % Ouery Match Length DB .3 6321 .1 144090 .9 174496 .4 232575 .2 2648 125159 174303 27913 62847 95282 159184 185263 174031 28777777777 28775777777 Score 513 613 613 613 510.8 510.8 510.8 510.8 26 26 26 Result No.

PAT 17-0CT-2001 Hur 3/15/99 Hw. linear DNA (bases 1 to 1745)
Williams L.T. and Morishita,K.
Promoter for VEGF receptor.
Patent: US 6445512-A 1 12-JUN-2001;
Location/Oualifiers AR157385 Sequence 1 from patent US 6245512. AR157385 AR157385.1 GI:16218320 Unknown. Unclassified. Unknown.

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL FEATURES

DEFINITION

RESULI 1 AR157385 LOCUS

ACCESSION VERSION KEYWORDS

ALIGNMENTS

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Indels
                              HUMES 1745 bp DNA linear Human gene for vascular endothelial growth factor
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                                                                                        growth factor receptor
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="placenta"
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/evidence=not_experimental
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ö PRI 14-APR-2000 receptor, Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1745) receptor Submitted (31-400-1995) Kaoru Morishita, Daiichi Pharmaceutical Submitted (31-400-1995) Kaoru Morishita, Daiichi Pharmaceutical Co. Ltd., Exploratory Research Laboratories 2; 1-16-13, Kita-Kasai, Edogawa-Ku, Tokyo 134, Japan (Tel:03-3680-0151(ex.372), Fax:03-5696-8718)
Location/Qualifiers /product-"vascular endothelial growth factor receptor" 180 240 739 300 799 360 420 559 GIECCAAGCAAGCGICAGIICCCCICAGGCGCICCAGGIICAGIGCCIIGIGCCGAGGGI 120 619 Gaps GCCGAAAAAGACACGGACACGCICCCTGGGACCIGAGCTGGTTCGCAGTCTTCCCAAAG 60 GCGGGAAGAGCAGGCAAGGGGAGACAGCCGGACTGCGCCTCAGTCCTCCGTGCCAAGAAC 241 ACCSTCGCGGAGGCGGGCCAGCTTCCCTTGGATCGGACTTTCCGCCCCTAGGGCCAGGC GGCGGAGCTICAGCCTIGTCCCTICCCCAGTITCGGGCGGCCCCCAGAGCTGAGTAAGCC GGGTGGAGGGAGTCTGCAAGGATTTCCTGAGCGCGATGGGCAGGAGGAGGGGCAAGGGCA 121 CICCGGIGCCIICCIAGACIICICGGGACAGICIGAAGGGGICAGGAGCGGCGGCACAGC Morishita,K., Johnson,D.E. and Williams,L.T. A novel promoter for vascular endothelial growth factor re (flt-1) that confers endothelial specific gene expression J. Biol. Chem. 270 (46), 27948-27953 (1995) .; 0 9; Length 1745;

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                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Wp:, WORMPEP; Information on the WORMPEP
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note-"LIMC4 repeat: matches 7645. .7820 of consensus"
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                                                                                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence is not the entire insert of clone RP11-9566 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-9566 is at 102119 in this sequence. The true left end of clone RP11-57H34 is at 59065 sequence. The true right end of clone RP11-57H34 is at 100
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note="MER5B repeat: matches 84. 178 of consensus"
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8655. 8771
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/hote="Alusx repeat: matches 1. .300 of consensus"
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13961. .14177
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4564, .14862
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note="MIR repeat: matches 2. .252 of consensus"
                                                                                                                                                      copies 4 mer gigt 100% conserved
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/hote-112 copies 3 mer tta 94% conserved"
9958. .10079
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15580. .15698
/note="7 copies 17 mer 74% conserved"
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15701
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/db_xref="taxon:9606"
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851. .979
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1. .102119
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/clone="RP11-95G6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRI 09-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL139005 102119 bp DNA linear PRI 09-MAY-2001
Human DNA sequence from clone RP11-95G6 on chromosome 13, corplete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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   860 GGGTGGAGGAGTCTGCAAGGAITTCCIGAGCGCGAIGGGCAGGGAGGGGCAAGGGCA 919
                                                             AGCACCTCCCCACGCGCGCTCGGCCCCGGGCCACCCGGCCTCGTCGGGCCCCGGCCCTCT
                                                                                                                                                                                                                              541 CCGIAGCCGCAGGGAAGCGAGCCIGGGAGGAAGAAGAGGGIAGGIGGGGAGGCGGAIGAS
                                                                                                                                                                                                                                                                                                                                                          1160 AAGGITATAAALCSCCCCCGCCCTGGCTGTTCATCGAGGTCCGCGGGAGGCTGGA
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epeat_region	15525. 15704 /note="20 copies 4 mer tott 87% conserved" 15708 16014
t_reg	ote-"Alusx repeat: matches 1308 of consensus" 02216126
epeat_region	ote="Alu 11117 0+6="Wit
t_reg	23. ,17897 te="Mirror repeat: matches 193. ,260 of considerations
repeat_region	34310023 5te="LZ repeat: matche: 56918137
t_regi	ote="3 copies 23 mer 87% conserved" 19418777
t_regi	4 . 19385 112 repeat: matches 2648 . 2701 of consens e="L2 repeat: matches 2648 . 2701 of consens
repeat_region repeat region	35019 ote="MIR alo 19
t_regi	ote="MIR repeat: matches 85258 o 84220921
epeat_region	note="M 0956
eat_regi	05. 121072 121072 The state of the state of the state of consense of the state of t
Ö	note="? 2892.
at_regio	note="Alur repeat: matches 1299 of consensus 514825236
epeat_region	note="MiR repeat: matches 52147 of consensus 723227532
epeat_region	note="Alusq repeat: matches 1313 o 937529442
epeat_region	te="34 co 023002 te="1,2 re
epeat_region	185731999 note="Mir repeat: matches 25141 of consensus"
epeat_region	583136016 note="MER3 repeat: matches 1208 of consensu
t_regi	789538193 note="Alusx r
repeat_region	ucs44u note="MIR n693 40
at regi	note="L2 re 7794 A219
t regi	2/34
t_regi	ote="MIR repeat: matches 77140 of consensus 93744142
t_regi	note="MIR repeat: matches 14262 of consensus? 417344831
repeat_region	ote="MER50 repeat: 95445088
repeat_region	ote="FLAM_C repeat: matches 2129 99246035
repeat_region	te="22 copies 2 mer ac 90% conserved" 96. 46035
epeat_region	oter 10 copies 4 mer acac 95% conserved:
epeat_region	ote="LiMB8 repeat: matches 23112594 of cons: 45447743
epeat_region	edt: matches I: .zyz 0
epeat_region	4899. 48761. ARCHITECTURE 2004:
repeat_region	: Macches I: .273 Of consensu

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                                                       50781. 51024

horte-"LIMBB repeat: matches 5028. 5274 of consensus"

51044. 51179

/note="8 copies 17 mer 66% conserved"

/note="11MB repeat: matches 5271. 6171 of consensus"

52293. 52577
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repeat: matches 3347. .5028 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCCGAAAAAGACACGGACACGCTCCCCTGGGACCTGAGCTGGTTCGCAGTCTTCCCAAAG 60
                 /note="AluJb repeat: matches 1. .285 of consensus" 50781: .51024
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                                                                                                                                                                                                                                                                                                                                                            /note-"Alusx repeat: matches 1. .308 of consensus" 54900. 54983
/note-".4 copies 2 mer gg 64% conserved" /note-".5506. .5506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="AluJo repeat: matches 1. .295 of consensus"
                                                                                                                                                                                                                                                                                                       54044. 54138
//note="MIR repeat: matches 46. .142 of consensus"
54435. 54742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.8%; Score 939.4; DB 9; Length 102119; 99.9%; Pred. No. 7.8e-144; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                   53786. 53900
/note="5 copies 23 mer 68% conserved"
53788. 53875
/note="22 copies 4 mer agga 68% conserved"
54044. 54138
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Best Local Similarity 99.99
Matches 940; Conservative
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CCGGACTGCGCCTCAGICCICCGIGCCAAGACACGCGCGCGGGGGGCGCGCCCAGCTICC 267
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artificial sequences.
1 (Eases I to 6316)
Olek A., Piepenbrock,C. and Berlin,K.
Diagnosis of diseases associated with
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AX251105
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Promoter of human flt gene encoding receptor type tyrosine kinase.
E10168
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 840)
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C12N15/09, A61K31/70, A61K48/00, C12N5/10, C12P21/02//C07#21/04,
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[⊥]
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/tissuc_type='placenta'
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/57...
/product='receptor type tyrosine kinase'
                                                                        GCGCGCCAGGCGGACACTCTCTCGGCTCCTCCCCGGCGGCGCGGCGGCGCTCGGAGCGGG
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Best Local Similarity 98.6%; Fred. No. 4.9e-99;
Matches 725; Conservative 0; Mismatches 5; Indels
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'note='Ets core motif'
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Patent: JP 1995289263-A 1 07-NOV-1995;
DAI ICHI SETTAKU CO LTD
ASS HOMO SEPIENS (human)
FN JP 1995289263-A/1
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/db_xref="taxon:9606"
269 c 336 g llE
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topology: Linear;
hypothetical: No;
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ACCESSION
VERSION
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Diagnosis of diseases associated with the cell cycle
Patent: WO 0169911-A 129 20-SEP-2001;
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4932 AAGGIIAIAAAICGIIIICGIIIICGGIIGIIIIIAICGAGGIICGCGGGAGGIICGGA 4993
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
a 255 c 1803 g 2758 t
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                                                            4992 GCGCGTTAGGCGGATATITITICGGTTTTTTTCGGTAGCGGCGGCGGTTCGGAGCGGG
                                                                                                                           5052 ITTCGGGGTTCGGGTGAGCGGTTAGCGGCGTTTGGCGGCCAGCATTATTCGGGGAAGT
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                             721 GCGCGCCAGGCGACACICCICCGGCTCCTCCCCCGCCAGCGGCGCGCGCGCTCGGAGCGGG
                                                                                              781 CICCGGGGCICGGGIGCAGCGGCCAGCGGGGGCCCIGGCGGCGAGGAIIACCCGGGGAAGI
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Diagnosis of diseases associated with signal transduction
Patent: WO 0200526-A 103 03-JAN-2002;
Epigenomics AG (DE)
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Pred. No. 1.7e-90;
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Best Local Similarity 78.2%;
Matches 736; Conservative (
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PAT 06-FER-2002
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/do.ansim="synthetic construct"

/do.aref="taxon:32630"

/note="chemically treated genomic DNA (Homo sapiens)"

255 c 1803 g 2768 t
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Diagnosis of diseases associated with cell signalling
Patent: WO 0202807-A 105 10-JAN-2002;
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Sequence 105 from Patent W00202807.
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DNA (Homo sapiens)"

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/organism="synthetic construct" /db\_xxef="texon:32830" /note="chemically treated genom: a 258 c 1805 q 2769 t

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Rabbrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Babrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnia, D., Bouck, J., Benton, J., Brankenburg, K., Bonnia, D., Bouck, J., Borton, P., Burkett, C., Burrell, K. L., Byrd, N. C., Chen, R., Carter, M., Cavazos, S. R., Chavo, J., Chavez, D., Chan, R., Chen, R., David, R., David, R., David, R., David, R., David, R., Douthwaite, K., J., Draper, H., Dugan-Rocha, S., Durbin, K. J., Earlado, O., Eddy, C. C., Escetto, R., Ernandez, R., Earlag, N., Endis, C., Haves, A., Hernandez, J., Harris, C., Hollins, B., Harris, C., Harris, C., Harris, C., Harris, C., Liaris, R., Harris, C., Lich, L., Korvah, J., Kovar, C., Katlovic, J., Kureshi, A., Ladid, R., Lewis, L., C., Lewis, L., Li, J., Li, Mahsehwari, M., Mapua, P., Martin, R., Martin, R., Martin, R., Marsey, E., Mahhiney, E., Miner, G., Miloer, M., Mil
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                                                                                                                                                 Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebraca; Euteleostomi;
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Web site: http://www.hgsc.bcm.tmc.edu/
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Center clone name: CH230-448N2
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AUTHORS
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/dos/Genbank.draft_data.html).
NOTE: This is a 'working draft' sequence it currently consists of 57 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are reported as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 160% of reads
Assembly program: Phrap; version 0.590325
Consens.s quality: 101711 bases at least Q40
Consens.s quality: 106747 bases at least Q30
Consens.s quality: 110016 bases at least Q20
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contig of 1667 b
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contig of 1051
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COMMENT

TITLE

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AF063657 4017 bp mRNA linear FKI 11-MAY-2001 HGGG sapiens vascular endothelial growth factor receptor (FLTI) MRNA, complete ods.
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Yu.Y., Whitney.R.G. and Sato,J.D.
Dienct Submissions
Submitted (66-WAY-1998) Adirondack Biomedical Research Institute,
10 old Barn Rd., Lake Placid, NY 12946, USA
Location/Qualifiers
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertecrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4017)

Herley,M.T., Yu,Y., Whitney,R.G. and Sato,J.D.

Characterization of the VEGF binding site c. t.e. Flt-1 receptor

Blochem. Blophys. Res. Commun. 262 (3), 731-738 (1999)

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/cell_type="endothelium"
/tissue_type="umbilical vein"
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                                                                                                                                                                                                                         Sequence 55 from Patent ..002055693.
Ax481481
Ax481481.1 G1:22316395
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1 915 c 903 g 963
                                                                                               DD 116205 ICITTGICCTAIGCAGA 116189
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Best Local Similarity 99.1%;
Matches 115; Conservative
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AF063657
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Best Local Similarity 80.23
Matches 158; Conservative
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Gaps

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3 (bases 1 to 7680)
Han, H.J., Fujiwara, T., Shin, S. and Nakamura, Y.
Dinucleotide repeat polymorphism in the 3' non-coding region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"NVSYWDTGVLLCALLSCLLLIGSSSGSKLKDPELSLKGTGHIMQ
AGGTLHLQCKGEAAHKWSLPEMYSKESERLSIIKSACGRNGKQFCSTLTLMTAQANHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEJGLLTCBATVNGHLYKT
NYLTHRQTNTIIDVQISTPRPVKLLRGHTLVLNCTAIIPLNTRVQMTMSYPDEKNKRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVRRRIDOSNSHANIFYSVLTIDKMONKDKGLYICRVRSGPSFKSVNISVHIYDKAFI
IVKHRKOOVLETVAGKRSYRLSMKVKAFPSPEVVWLKJGLPAIEKSARYLIRGYSLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDVIEEDÄGNYTILLSIKOSNVFKNLTATLIVNVFÖLIFEKNYSSPOPALYELÖSEN
ILTCTATORIPORTIKWENHICNNHHESERADECSNNEESFILDADSNMGKRIESITOR
MAITEGKNKMASTLYVADST ISGIYLOLASNKYGTVGKNIEFY ITDVPNGEMULEKN
PTEGEDLKLSCTVNKFLYRDVTHILLRIVNNRTMHYSISKOKMAITKEHSITLNITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVSLQDSGTYACRARNYTGEEILQKKEITIRDQEAFYLLRNLSDHTVAISSSTTLDC
HANGVPEPQITWFKNNHKIQQEPGILLGPGSSTLFIERVTEEDEGVYHCKATNQKGSV
ESSAXLFVQGTSDKSNLELITLTCTCVAATLFWLLIILIRKWKRSSSEIKTDYLSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVAVKALKEGATASEYKALMTELKILTHIGHHINVVNLLGACTKOGGPLAVIVEYCKY
GNLSNYLKSKRDILFFLNKDAALHMEPKKEKMEPGLEGGKKPRLDSVTSSESFASSGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAFEYSTPETYQIMIDCWHRDPKBRPR
FAELVEKLGDLLQANVQQDGKDYIPINAILIGNSGFIYSTPAFSEDFFKESISAFKFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGSSDDVRYVNAFKEMSLERIKTFEELLPNATSMFDDVQGDSSTLLASPMLKRFTWTD
SKPKASLKIDLRVISKSKESGLSDVSRPSFCHSSCGHVSECKRRFTVDHAELERKIAC
CSPPDVNSVVLYSTPPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFYSCKYLAVPISKKKETESAIYIFISDIGRPFVEMYSEIPEIIHMTEGRELVIPCRV
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                                                                                                                                                                                                              Data kindly reviewed (20-JUL-1990) by Shibuya M.
Locallon/Qualifiers
1. 7680
                                                                                                                                                                                                                                                                                                                                                                                                                                             250. .4266
/note-"flt gene product (AA 1-1338)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SWISS-PROT:P17948"
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                                                                                                                                   Genet. 2 (12), 2204 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/protein_id="CAA35946.1"
/db_xref="G1:31432"
                                                                                                                                                                                                                                                                                         /organism-"Homo sapiens"
/db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="placenta"
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                                                                                                                                                                                                                                                                                                                                                                                            /clone="3-7, 3-5"
                                                                                                                                                                                                                                                                                                                                            /chromosome-"13"
/map="13q12"
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TITLE
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MAIIESGNKKMASTLVVADSRISGIYICIASNKVGTVGRAISFYTTDVPRGFHYNLEKN
PTEGEDLKLSCTVNKFLYRDVTWILLRTVNNRTMHYSISKQKMAIITREHSIILNITIN
NVSLODSGTYAGRANVYIGEELLQKKEITIHDGEAPYLLKNLSDHTVAISSSITLCE
HANGVPEPQITWFKNNHKIQQEPGIILGFGSSTLFIEBVTEEDEGGYYHCKAINGSGV
                                                                                                                                                                                                                                                                                                                                                    SVRRIDGSNSHANIFYSVLTIDKMONKDKGLYICKVRSGPSFKSVNISVHIYDKAFT
TVKHRKQQVLETVAGKRSYRLSMKVKAFPSPEVVWIKDGLPATEKSARVLIRGYSLII
KDVTEEDAGNYTILLSIKQSNVFKNLTATLIVNVKPQIYEKAVSSFPDPALYFLGSRQ
                                                                                                                                                                                                                         /trānslation="wvsywdtgviicallsciilisssosklkdpelsikdiodhimg
Aggylhlqorgeaahkwslpewvskeserlsiiksacgrngkgestlilkagamht
GFYSCKYLAVPTSKKKETESAIYIFISDIGRPFVEWYSEIPEIIHMTEGRELVIPCRV
TSPWITVTLKKFPFDTIIPDGKRIIMDSRKGFIISNATYKEIGLITCEAIVWHTKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BSSAYLTVQGTSDKSNLELITLTCTCVAATLFWLLLTLF1RKMKRSSSE1KTDYLS11
MDPDEVPLDEQCERLPYDASKWEFARERLKLGKSLGRGAFGKVVQASAFGIKKSPICR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKERPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGSSDDVRYVNAFKFMSLERIKTFEELLPNATSMFDDYOGDSSTILLASPMLKRFTWTD
SKPKASLKIDLRVTSKSKESGLSDVSRPSFC!!SSCG!!VSEGKRRFTYD!|AELERKIAC
                                                                                                                                                                                                                                                                                                                               NYLTHRQTNTIIDVQISTPRPVKLLRGHTLVLNCIATTPLNTRVQMTWSYPSEKNKRA
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GNLSNYLKSKRDLFFLNKDAALHMEPKKEKMEPGLEQGKKPRLDSVTSSESFASSGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDKSLSDVEEEEBSDGFYKEPITMEDLISYSFQVARGMEFISSRKCIHRDIAARNILL
SENNVYKICDFGLARDIYKNPDYVRKGDIRLPLKWMAPESIFDKIYSTKSDVWSYGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAELVEKLGDLLQANVQQDGKDYIPINAILTGNSGFTYSTPAFSEDFFKESISAPKFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Gominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (02-JaN-1989) Shibuya M., Institute of MedfCTl Science,
University of Tokyo, 4-6-1 Shirokane-dai, Minato-ku, Tokyo 108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3173 ATACTGACTTCCTCTGAAATGGATGGCTCCTGAATCTTTGACAAAATCTACAGCA 3232
                                                                                                                                                   /product="vascular endothelial growth factor receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 CCAAGAGGGACGTGTGGTCTTACGGAGTATTGCTGGGGAAATCTTCTCCTTAGGT 181
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Shibuya,M., Yamaguchi,S., Yamane,A., Ikeda,I., Τοjο,A.,
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99.1%; Pred. No. 3.5e-23;
tive 0; Mismatches 1;
                                                                                                   tyrosine kinase"
                                                                                                                                                                           /protein_id="AAC16449.1"
/db_xref="GI:3132831"
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                                                                     /gene="FLT1"
/note="VEGFR;
                                                                                                                           /codon_start-1
                  /gene="FLT1"
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Shibuya, M.
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X51602.1 GI:31431
flt gene; fms-relate
Homo sapiens.
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Matches 115; Conservative
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                                                .4017
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James, R.A., Rouse, G., Wu, Z.,
Buckley, D., Kibukawa, M., Raymond, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24786 ACITGACITCCTCTGAAAIGGATGGCTCTIGAATCTATCTIGACAAAAICIACAGCACC 24727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC104439 197279 bp GNA linear PRI 20-JUN-
HONG sapiens chromosome 3 clone RP11-793E15, complete sequence.
AC104439 AC024739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macmalia: Eutheria: Primates; Catarrhini; Hominidae: Homo. [ [bases 1 to 19729] 
Kav., K., Olson, M.V., Zhou, Y., James, R.A., Kouse, G., Wu, Z
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201474 201573: gap of 100 bp
201574 202307: contig of 734 bp in length
20208 20407: gap of 100 bp
202408 204378: contig of 2471 bp in length
204879 204978: gap of 100 bp
204879 213531: contig of 8553 bp in length
215532 218503: contig of 4478 bp in length
21810 218209: gap of 100 bp
                                                                                                                                                                                                                                                                                          ap of 100 bp
contig of 53424 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18209; gap of 100 bp 2519800; contig of 1591 bp in length 15900; ap of 100 bp 220965; contig of 1065 bp in length.
                                                                                                                                                                                                                                                                                                                                      89052 189151: gap of 100 bp
89152 189476: contig of 325 bp in length
89477 189576: gap of 100 bp
89577 191375: contig of 1799 bp in length
                           7955; gap of 100 bp conting of 1428 bp in length 5948; gap of 100 bp langth 131747; contig of 2264 bp in length
                                                                                                                           1847: gap of 100 bp 13216: contig of 469 bp in length 2416: gap of 100 bp 13455: contig of 2039 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of 100 bp scontig of 9998 bp in length
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  127855: contig of 5921 bp in leagth
                                                                                                                                                                                                                                                            contig of 972 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.7%; Score 104.4; DB 2;
ilarity 54.7%; Pred. No. 3.4e-20;
Conservative 0; Mismatches 6;
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                                                                                                                                                                                                                                      100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP6-32923"
                                                                                                                                                                                                                                                                                             gap of
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ACI04439.2 GI:21490240
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29484 1317
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34556 1355
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Matches 108: Conserv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp
                                                                                                                           the transcriptional map of the common eliminated region 1 (C3CER1)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                      Submitted (01-APR-2001) Kiss H., Microbiology and Tumorbiology Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
                                                                            Kiss, H., Yang, Y., Kiss, C., Andersson, K., Klein, G., Imreh, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-6800 bp) and clone RP6-188911 (partially, 1-108303 bp). The sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone RP6-32g23 (31212-220965 bp), clone RP6-146e1 (partially.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in order and the gaps between them are represented by 100 Ns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by the finished sequence as soon as it is available and the accession number will be preserved.

1 11731: contig of 11731 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35628-189051 bp Contig 18: 189152-189476 bp Contig 19: 89577-191375 bp
ontig 20: 191476-201473 bp Contig 21: 201574-202307 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .17756-118727 bp
contig 10: 118828-121834 bp Contig 11: 121935-127855 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61679-97342 bp Contig 8: 97443-117655 bp Contig 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61579 61678: gap of 100 bp
61679 97342: contig of 35664 bp in length
97343 97442: gap of 100 bp
97443 117655: contig of 20213 bp in length
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55059: contig of 12699 bp in length
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26319 28347: contig of 2029 bp in length
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55160 61578: contig of 6419 bp in length
                                                                                                                                                                             . Hum. Genet. 10 (1), 52-61 (2002)
                                                                                                                                                                                                                                                         (bases 1 to 220965)
                                                                                                                                                                                                                                                                                                              Direct Submission
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12361 550
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                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
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                                                                            AUTHORS
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0; Gaps

6; Indels

Length 220965;

2600 others

linear PRI 20-JUN-2002

Direct Submission Submitted (11.0EC.2001) Genome Center, University of Washington, Box 35116, Seattle, WA 98195, USA Raul,R.K., Olson,W.Y., Zhou,Y.Y., James, M.A., Rouse,G., Wiw,Z., and Haugen E.D. Submitted (10.0WG. Very 100.0 E.M.) Box 10.0 E.M. Strukkawa, W., Raymond,C. Submitted (10.0WG. Very 100.0 Genome Center, University of Washington, Box 35116, Seattle, WA 98195, USA On Jun 20, 2002 this sequence version replaced gi:1746621. Center Code: UWGC Center Supering Code: UWGC Center Code: UWGC Center Code: UWGC Center Code: UWGC Center Code: UWGC Center Code: UWGC Center Code: UW
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JOURNAL Oncogene 9 (9), 2683-2650 (1994)  MEFERENCE 2 (bases 1 to 4734)  AUTHORS Shibuya,M. JOURNAL Unpublished  AUTHORS Shibuya,M. JOURNAL Shibuya,M. JOURNAL Shibuya,M. JOURNAL Shibuya,M. JOURNAL Submission  JILLE Direct Submission  JOURNAL Submission  Fast:03-649-549-549-549-5550,  FEALURES.  Source 1. 4734		SVEHEKOQVETTAGKESHELSMYKAFPSPEVWALKDOPATEKSARVSUGYSLII KDVTAEDDAGDTILLGIKQSKIFRNIJATILVWKPQIYEKSYSLPSPEVPLGSRQ VLICTYYGIPOPTHUGHYHHSKERNDECEGSESFILDSSANIGRHIEGITOR MAVIGTHATVYSTLYVADSRTPGSTSCRAPNKIGTVERDIRFYYDDVRGFHYSLEKI PTGSDLKKLSCVVSKFLYRDTWILLETTVANRAHHSISTROMATTODSTILLUIK NVSLBDSGTYACRANIYTGEBILKRTEVIVADERFLIGNISDBGYYRCRATNOKGVV BSAYLTVQGTSARSNITTILTCTCAVALTELLILLIETRKRSSESYTLDC QARQYPAPOITWRNNHKIQOPPGILLGROAALTELLILETRKRSSESYTLDC GARGYPAPOITWRNNHKIQOPPGILLGROAALTELLILETRKRSSESYTLDC GARGYPAPOITWRNNHKIQOPPGILLGROAALTELLILETRKRSSESYTADC GARGYPAPOITWRNNHKIQOPPGILLGROAALTELLILETRKRSSESYTADC GARGYPAPOITWRNNHKIQOPPGILLGROAALTELLILTETRKRSSESTTSGGT GARGYPAPOITWRNNHKIQOPPGILLGROAALTELLILETRKRSSESTTSGGT GARGYPAPOITWRNNHKIQOPPGILLGROAALTELLILETRANSSANGTRKRSSEPTC GALSVLKKSRDFCLNNDAALHDERFREKKEREDDEGOCKPREDSSTSGTOG EDKSVSBDVEGGEDSYSEISKQPLTMEDLISTSFOVARGHELLSSRCIHRDLAANHILL SENNVVKICDFGLARDIYKNPDYVRGDTRLPKMAPESIFDKVYSTKSDVWSYGVL LWEITSLGGSSPPGVQMDEDCORPHYBERATAFELIGAULDCHARDRERPR FAELVEKLGDLLQANDOCKDYIPLNAILTRNGFTISTPLKRFWHT SGSSDDVRYVNAFKFREIRIKTFEELSPNAISMFEDSTLFSPLKRFFWFT FRENKRSSPPRA FRENKRSSRVILLRTSKSREAGLSDLFGGPSCCGHIRPVRGEDDPELGKSSCCG PPPPDYNSVLYSSPPA"  1271 a 1263 c 1209 9 991 L	Query Match Best Local Similarity 89.6%; Pred. No. 1.2e-17; Matches 103; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Gy 66 AGACICGACITCCTCAAATGGATGGCTCCTGAATCTTIGACAAAATCTACGCA. 125 Illillillillillillillillillillillillilli
237       <800	1174     1145     2152     2160     1479     1476       7876     8291     249     <800	Query Match Best Local Similarity 93.9%; Pred. No. 1e-15; Matches 107; Conservative 0; Mismatches 7; Indels 0; Gaps 0; QY 68 ACTGGACTTCCTCGAAATGGATGGCTCCTGAATCITTGACAAAATCTACAGCACC 127 III	receptor; VEGF/VPF -binding; Fms/Kit/FDGF receptor ityrosine kinase receptor. Rattus norvegicus (strain Fisher F341) adult lung an to mRMA, clone 44/7-4/3-8.  Rattus norvegicus (strain Fisher F341) adult lung an to mRMA, clone 44/7-4/3-8.  Rattus norvegicus (brondata; Craniaia; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus (sites)  Rattus (sites)  Rattus (soconmunication system between hepatocytes and sendothelial cells in liver through vascular endothelial factor and Fit tyrosine kinase receptor family (Fit-KDR/FIK-1)

3472 CCAASAGCGATGIGIGGICCIATGGCGTGTIGCIGIGGGAGATCIICICCTIAGG 3526

Di:

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TSPNVTVLKKEPPDTLTPDGQRITWDSRRGFIIANATYKEIGLLNCEAVNSHLYTY
YLTHRQTNTILDVOIRPSSPVRLLCGGTLVLNCTATTELNTRVQMSHNYPGKAITRAS
YLTHRQTNTILDVOIRPSSPVRLLCGGTLVLNCTATTELNTRVQMSHNYPGKAITRAS
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VKHRKQPVOBTTAGRRSYRLSRKVKAFPSPETVHHKKQSPATIKSAYTUHGYSLIT
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SLEDSGTYARRARTYTGEDIRKTPVLVROSFAHHLLONISNFVSSGSTILLCCA
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AAYLTVQGTSDKSNLELITLYTTCVAATLEMILIILFIRKLKRSSSEVKTDYLSIIND
PDEVPLEDGCERLEVDASNWEFREREKLKLKSLEGGAGRAVOASASTSTKSPTCRIV
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LSNYLKSKRDLFCLNKDAALHNELKKESLEPGLEGGGCKPRLDSVSSSSVYSSSFFEDR
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/db_xref="SWISS-PROT:P35969"
/translation="MVSCWDTAVLPYALLGCLL.IGYGSGSKLKVPELSLKGIGHVWQ
AGQILFLKCRGEAAHSWSLPTTVSQEDKRLSITPPSACGRDRRQFCSTLTLD.AGANH
TGLYTCRYLPTSTSKKKKAESSIYIFYSDAGSPFIRMHIDPKY
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NVVKICDFGLARDIYKNPDYVRRGDTRLPLKWWAPESIFDKVYSIKSDVMSYGVLLWE
     ROD 07-JUL-1954
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KASMKIDLRIASPRKEAGLSDLPRPSFCFSSCGHIRPVQDDESELGKESCCSPPPDYN
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                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostcon; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 5482)
Choi.K., Wall.C., Hanratty.R. and Keller,G.
Isolation of a gene encoding a novel receptor tyrosine kinase from differentiated embryonic stem cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (05-JUL-1994) Chol K., 1400 Jackson St. K501, Denver Co
        linear
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/protein_id="CAA55311.1"
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        mRNA
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5482 bp
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                                                                                                                 EmRK2 gene; receptor kinase.
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                          M.musculus EmRK2 cDNA.
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Choi, K.
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                                                                                                                66 AGACICGACITCCICIGAAAIGGAIGGCICCTGAAICIAICITIGACAAAAICTACAGCA 125
                                                                                        Gaps
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                                               31.8%; Score 95.8; DB 10; Length 5482; 89.6%; Pred. No. 1.2e-17; tive 0; Mismatches 12; Indels 0;
1369 g 1203 t
1446 c
                                                                               Matches 103; Conservative
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Best Local Similarity
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QQ A

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MUSKIKB 605-AUG-1993
Mus musculus receptor tyrosine kinase (FLI) mRNA, complete cds.
107297
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ASI RORIDBSHSHNIVFHSVLKI INNVESRDKGLYTCRVKSGSSFOGSFUSVYVPEKGK
ISVAKRORVQETTRGRRSYRLSHKVKRFPSPEIVHIKTGSSPATIKKSARLVHGYSLI
IKDYTTEDRGPVTILLIGHROSHERMINATILIVVKPQIYEKSVSSLFPSPLYPHGSR
QVLTCTYVGIPPRTITMINHIPKERNYPECTINESSTILDBSSNIGNRIESIS
RMTVIEGINKIVSTLVVADSQIPGIXSCRAFNKIGIVERNIKFYYTDVPNGFHYSLER
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VESAAYLIVQGTSDKSNLELITLICTCVAATLEWLLILFIERIKKRSSSBWKTDYLSI
IMDPDEVPLDEQCERLPYDASKWEFARERLKLGKSLGRGAFGKVVQASAFGIKKSPTC
RIVAVKMLKBGATASEYKALMTELKILTHIGHHINVVNLLGACIKQGGFLMVIVEDCK
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FAELVEKLGDLLQANVQQDGKDYIPLNAILIRNSSFIYSIPIFSEDLFKDGFADPHFH
SGSSDDVRYVNAFKFWSLERIKIFEELSPNSISMFEDYQLDISILLGSPLIKRFTWIE
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KNVSLEDSGTYACRARNIYIGEDILRKTEVLVKDSEARHLLQNLSDYEVSISGSTTLD
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EDRSVSDVEGDEDYSEISKQFLTMEDLISYSFQVARGMEFLSSRKCIHRDLAARNILL
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AGØILFLKCRGEAAHSWSLPTIVSQEDKRLSIIPFSACGRDNRQFCSTLILDTAQANH
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VTSPNVTVILKKFPFDTLIPDGQRIIMDSRRGFIIANAIYKEIGLLNCEATVNGHLYQ
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Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 6055)
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                                                                                                                                      L07297,1 GI:293782
receptor protein tyrosine kinase.
Mus musculus (strain C57BL/63, sub_species domesticus) cDNA to
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/protein_id="AAA46078.1"
/db_xref="G1:293783"
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/db_xref="taxon:10090"
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/strain="C57BL/6J"
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SGSSDDVRYVNAFKFMSLERIKTFEBLSPNSTSMFEDYQLDTSTLLGSPLLKRTWTB
TRPKASMKIDLRTASKSKEAGLSDLPRPSFCFSSCGHIRPVQDDESELGKESCCSPPP
DYNSVVLYSSPPA"
MPAEGEDLKLSCVVNKFLYRDITHILLRTVNNRIMHHSISKQKMATTQDYSITLNLVI
KRYGLEDSGSTYACRARNYTGEDILEKTRYEVYRDSEAPHLLQNLSDYFRSTIG
CQARGUPARQITHEKNHHKIQQEPGILLGPGNSTLEIERYTEEDEGVYRCRATHOKGA
VESNAYLYVQGISDKSNLELITLICTCVAATLFHLLILFFIRKLKRSSSEVKTDYLSI
                                                                                    IMDEDEVPLEGGCERLPYDASKWEFARERLKIGKSLGRGÅFGKVVQASAFGIKKSPTC
RIVAKMIKEGATASERKALMERILITHIGHLNVVLILGACKYGGOLMUTVEKCK
RIVAKMIKEGATASERKALMERILKITHIGHLNVVLILGACKYGGOLMUTVEKK
FORLSNYLKSRFD.FCLLMOALHMERKKESLEPGLEGGGKPRLDSVSSSSY
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LWEIFSLGGSPYPGVQMDEDFCSRLKEGMRMKIPEYAIPEIXQIMLDCWHKDPKERPR
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2848. .2961
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2962, .3050
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2503. .2609
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TRANSLYETKURTARSTSTITLDIAGANG
VESPNYTVYLKKFPFDTLTPDGRGTTWOSRRGFILANATYKEIGLLNCEATVNGHIYO
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ASTRORIDRSHSHNNYFHSVLKINNYESRDKGLYTCRVKSGSSFQSFNTSVHVYEKGF
ISVKHRKOPVOETTAGRRSYRLSMKVKAFPSPEIVMLKDGSPATLKSARYLVHGYSLI
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QVLTCTVYGIPRPTITWLMHPCHHNHSKERYDFCTENEESFILDPSSNLGNRIESISQ
RMTVIEGTNKTVSTLVVADSQTPGIYSCRAFNKIGTVERNIKFYVTDVPNGFHVSLEK
                                                                                                                                                                                  ROD 30-JUL-2002
                                                                                                                                                                                                                                                                                         Mus musculus (strain:C57/b) lung cDNA to mRNA, clone_lib:mouse lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (31-0cT-1996) Kunio Kondo, The Institute of Medical Science, The University of Tokyo, Department of Clinical Oncology; 4-6-1 Shirokanedai, Minato-ku, Toky 108, Japan (Tel:+81-3-5449-5622, Fax:+81-3-5449-5428)
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibuya,M. Genomication of the fit-1 gene encoding for Vascular Genomic organization of the Fits receptor 1 suggests an intimate Endothelial growth factor (VEGF) receptor 1 suggests an intimate evolutionary relationship between the 7-1g and the 5-1g tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                             Finnerty,H., Kelleher,K., Morris,G.E., Bean,K., Merberg,D.M., Kriz,R., Morris,J.C., Sookdeo,H., Turner,K.J. and Wood,C.R. Molecular cloning of murine FLT and FLT4 Oncogene 8 (8), 2293-2298 (1993)
                         Kondo, K., Hiratuka, S., Subbalakshmi, E., Matsushime, H. and
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                                                                                                                                                                                    linear
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                                                                                                                                                                                  D88689 6275 bp mRNA Mus musculus mRNA for flt-1, complete cds.
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/clone="MD-9-11"
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1. 6275
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1. .251
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Gene (1998) In press
3 (bases 1 to 6275)
Kondo, K.
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Mus musculus
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1 (bases 1 to 666)
Scholz, I.D. and Segar, J.L.
Stholz, I.D. and Segar, J.L.
Submitted (09-FEB-2000) Pediatrics, University of Iowa, 200 Hawkins Drive, Iowa City, IA 52242, USA
Location/Qualifiers
1. 666
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Shibuya,M.
Shibuya,M.
Direct Submission
Submitted (11-JU1-2001) Masabumi Shibuya, University of Tokyo,
Institute of Medical Science, 4-6-1 Shirokane Jai, Minato-ku, Tokyo
108-8639, Japan (E-mail:shibuya@ims.u-tokyo.sc.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="varameflssrcihrdlaarnillseknvvkiodeglardiyk
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gkdy iplinallitgonsafiysipafsedffgedisafkrisglobungvvvarbhalti
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Mammaila, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Boyidae: Caprinae, Ovis.
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Eukaryota, Metazoa, Chordata, Craniata, Vertezrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamaguchi,S., Iwata,K. and Shibuya,M.
Soluble Flt-1 (soluble VECFR-1), a potent natural antiangiogenic molecule in mammals, is phylogenetically conserved in avians Blochem. Biophys. Res. Commun. 291 (3), 554-559 (2002)
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Pred. No. 3.5e-17;
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                           ovis aries Flt-1 mRNA, partial cds. AF233077
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Best Local Similarity 88.7%;
Matches 102; Conservative (
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3744. .3886
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/number=26
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/number-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAVTLKKIPRETLIPDGKTIIMDNMRGPRIPEATYRFIGLLSCETTIGGHXVSTKYLT
HRETNTIFDIKLSTPRLVKLLKGDSLAINCTVKAAMNTRVQMTWTYPGEAWKR3SVTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEQCECLPYDASKWEIARERLKLGKSLGHGAFGKVVQASAFGIKKSPTCRIVAVKALK
EGATASEYKALMTELKILIHIGHHLNIVNLLGACTKNGGPLMVIVEYCKYGNLSNYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ICDFGLARDIYKNPDYVRKGDARLPLKWMAPESIFDKIYNTKSDVWSYGVLLWEIFSI.
GASPYPGVQIDEDFCSKLKEGTRMRAPEQATEEIYQIMLDCWRSNPNERPWFSELVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGDLLQASVQQEGKDYIPLDTIFTAESGFPPASDPĪCNEKFPVPSPNCRSTERARYIN
TFKIKPPQRIKTFEELPIKEKLVFNDYQADSGMVLASEELKRFTWTGSKQKWTLFPGMK
GVSRSKESGLSGITKPRSFCSFSCDQLSESKRRYTYGNTVLEKMKACHSPPPDYSSVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKRNFFSPTKDPSLQGELMKDKKGIEPVEGKKQRLASVTSSESFASSGFQEDKSLSDA
EEDEEDAAELYKLPLIMEDLISYSFQVARGMEFLSSKKCIHRDLAARNILLSENNVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVERSNLELITLICTCVAATLEWLLLTLFIRKLKRPYFSETKTNHYLSIIMDPDEVPL
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                                                                                                                                                                                                                                                                                                                                        /product="vascular endothelial growth factor receptor-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 29.2%; Score 88; DB 5; Length 4272; l Similarity 86.6%; Pred. No. 2.5e-15; 97; Conservative 0; Mismatches 15; Indels
5449-5550, Fax:81-3-5449-5425)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                          fms-like tyrosine kinase-l"
                                                                                                                                     /tissue_lib="whole embryo"
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                                                                                                                                                                                     /gene="vegfr-1"
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                                                                                                                                                                                                                                                                                                                        /codon_start=1
        Tel:81-3-5449-5550,
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TITLE
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                                  FEATURES
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Swr. SWISSPROT? IT:, TREMBL, WP:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
humquery&sanger.ac.uk Clone requests: clonerequest&sanger.ac.uk On May 25, 2002 this sequence version replaced g1:20520452. During sequence assembly data is compared from overlapping clones. Martie differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 189669 CICITITIGCCCACCCAGGCCCGACTICCICTGAAATGGAIGGCCCCCGAGAGCAICIT 189728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-58El3 is from the RPC1-23 Mouse PAC Library constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 211330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.8%; Score 80.6; DB 10;
67.7%; Pred. No. 4.1e-13;
Live 0; Mismatches 54;
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| 45513:c 46613 g 55380 t
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/organism-"Mus musculus"
/db_xref≈"taxon:10090"
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Location/Qualifiers
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Matches 113, Conservative
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223
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                                               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)750-5050
TELEFAX: (212)869-5741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEGJENCE CHARACIERISTICS:

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10 US-05-866-510-3 110 US-09-866-510-5 12 US-09-866-510-5 12 US-09-866-510-5 13 US-09-9554-456-1593 140 US-09-954-456-1593 150 US-09-956-150-13 150 US-09-866-510-13 150 US-09-960-152-4253 150 US-09-960-152-1442 150 US-09-960-152-1442 150 US-09-960-152-127 150 US-09-960-152-127 150 US-09-960-152-1082 150 US-09-960-152-127 150 US-09-960	9/193,829 9/4 : A. 30,742 ER: 7683-
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Patent No. US20020072077Al
GENERAL INFORMATION:
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ADDRESSEE: Imclone
SIREET: 180 Varick
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ZIF: 10014
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Pred. No. 5.9e-200;
0; Mismatches 575; Indels
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                                                                                         NAME/KEY: CDS
LOCATION: 286..4386
SEQUENCE DESCRIPTION: SEQ ID NO:
LENGTH: 5470 base pairs
                   TYPE: nucleic acid
STRANDEDNESS: unknown
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65.0%;
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APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: IOTIPOTENT HEMATOPOIETIC SIEM CELL
RECEPTORS AND THEIR LIGANDS
1818 TITGCIICAAGCAAATGIACAACAGGATGGIAAAGACTACAT 1859
                           Systems Incorporated
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MEDIUM TYPE: Floppy disk
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2550 CATTCTCGTACGGACCGTTAAGCGGGCCAATGAAGGGAACTGAAGACAGGCTACTTGTC 2609
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                                              CAACCACAAAATACAACAAGAGCCTGGAATTATTTAGGACCAGGAAGCAGCACGCTGTT 500
                                                                                                                                                                                           561 GGGCTCTGTGGAAAGTTCAGCATACCTCACTGTTCAAGGAACCTCGGACAAGTCTAATCT 620
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                                                                   AACAGINGCCGICAAGAIGIIGAAAGAAGAACAACACACACAGCAGCAGCAGCCCICAI
                                                                                                                   621 GGAGCIGATCACTCTAACATGCACCTGTGGGCTGCGACTCTCTGGCTCCTATTAAC
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COMPUTER: IBM PC compatible
OPERAINS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Batentin Release #1.0, version #1.25
CURRENT APPLICATION DAIA:
APPLICATION MARE: US/09/919,408
FILING DAIE: 31-Jul-2001
CLASSIFICATION: <URNOwn>
PRIOR APPLICATION: <URNOwn>
FILING DAIE: <URNOwn>
FILING DAIE: <URNOwn>
                                                                                                                                                                                 APPLICATION NUMBER: US 07/906,397
FILLING DAFE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US PCI/US92/02750
                                                                                                                                                                                                                                                                                                               FILING DATE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
                                                                                                                                                                                                                                                         APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
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REGISTRATION NUMBER: 28,601
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TELEFAX: 212-645-2054
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208..264
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265..4308
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STRANDEDNESS: double
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                                                                                   1638 TGGGTCTCCATACCCAGGAGTACAAATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGG
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TITLE OF INVENTION: TOIIPOIENT HEMATOPOIETIC STEM CELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 1818 TITGCTICAAGCAAATGTACAACAGGATGGTAAAGACTACAT 1859
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APPLICATION NUMBER: US/07/977.453
FILING DATE: 192-11-19
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
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FILING DAIE: <UNKNOWN>
APPLICATION NUMBER: US/09/021,324
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FILING DAIE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
TITM DAIE: 24-DEC-1991
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APPLICATION NUMBER: US 07/728,913
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APPLICATION NUMBER: US 07/579,666
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09872135
Patent No. US20020115545Al
GENERAL INFORMATION:
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ADDRESSEE: ImClone
STREET: 180 Varick
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US-09-872-136-5
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2070 CAICLIGATIGEGGATIICAGAATGCCICTCIGCAGGACCAAGGCGACIATGTIIGCIC 2129
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Pred. No. 1.7e-199;
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                                                                            NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-
IELECOMMUNICATION: INFORMATION:
TELEPHONE: 212-645-1405
IELEFAX: 212-645-1405
    02-APR-1991
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SEQUENCE CHARACTERISTICS:
LENGTH: 5406 base pairs
ITYPE: nucleic acid
STRANDEDNESS: double
FILING DATE: 02-APR-199
AITORNEY/AGENT INFORMATION:
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265..4308
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65.08;
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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Matches 1080; Conservative
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798 TGCCAGCAAGTGGGAGITTGCCCGGGAGAGACTTAAACTGGGCAAATCACTTGGAAGAGG 857
                                                                                                                      918 GACTGTGGGCTGTGAAAATGCTGAAAGASGGGGCCACGGCCAGCGAGTACAAAGCTCTGNT 977
                 2790 AACAGTAGCCGTCAAGATGTIGAAAGAAGCAACAACACACAGGGAGCATCGAGCCTCAT
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Wood, William I.
IIILE OF INVENIOR: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk computer: ISM PC compatable OPERATING SYSTEM: PC-DOS/MS-DOS SOFIWARE: WinPatin (Genentech)
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Local Similarity 58.7%; Pred. No. 4.6e-150;
nes 981; Conservative 0; Mismatches 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,610
FILING DATE: 17-0ct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                   SIREET: 460 Point San Bruno Blvd CITY: South San Francisco SIATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DAIE: 1996-MAY-23
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
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REGISTRATION NUMBER: 40,378
Sequence 31, Application US/09982610 Patent No. US20020146420A1 GENERAL INFORMATION:
                                                                       Genentech, Inc.
Bennett, Brian D.
Goeddel, David
Lee, James M.
Matthews, William
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                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
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STRANDEDNESS: Single
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SEQUENCE CHARACTERISTICS:
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                                                                       APPLICANT:
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                                                           1552 TCTTTGACAAAATCTACAGGACGAGGAGGTGTGGGTCTTACGGAGTATTGCTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,610
FILING DATE: 17-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 04-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno I
CIT: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 45, Application US/09982610 Patent No. US20020146420al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee, James M.
Matthews, William
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Wood, William I
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STRANDEDNESS: Single
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INFORMATION FOR SEQ ID NO: 45:
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                                         9108
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                                         DB 10; Length
                                                                  Indels
                                                                  679:
                                      Score 541.6; DB 10;
Pred. No. 7.2e-150;
0; Mismatches 679;
 45:
; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-982-610-45
                                                 Rest Local Similarity 58.7 Matches 981; Conservative
                                    Query Match
Best Local
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                                       1202 AAGGCAAGAAACCAAGACTAGATAGCGTCACCAGCAGCGAAAGCTTTGCGAGCTCCGGCT 1253
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Rood, William I.
IILE OF INVENTION: PROTEIN IYROSINE KINASE AGONISI ANTIBODIES
                                                                                                                                                                                                          1322 AGGAGCCCATCACTATGGAAGATCTGATTTCTTACAGTTTTCAAGTGGCCAGAGGCATGG
                                                                                                                                                                                                                                                                                              1382 AGIICCIGICIICCAGAAAGIGCAIICAICGGGACCIGGCAGCGAGAAACAIICIIITAI
                                                                                 3859 TCGCCAGGCIGGATCGGAGGCGGCCGGGAGCAGCGACAGGGTCCTCTTCGCGGGGTTCT
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPPERING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Geneantech)
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STREET: 460 Point San Bruno Blvd
CIIY: South San Francisco
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Matthews, William
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Bennett, Brian D
Goeddel, David
3808 GCGCGGAGAGTCICCCGA----
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CORRESPONDENCE ADDRESS:
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Patent No. USzvoz.
TWFRAL INFORMATION:
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Pred. No. 3.5e-73;
0; Mismatches 172;
                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P0821P3PCT TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1994
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/982,610
FILLING DATE: 17-Oct-2001
CLASSIFICATION: <Unknown>
                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,648
FILING DATE: 1996-MAT-23
APPLICATION NUMBER: 08/222616
FILING DATE: 04.APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,379
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                            LENGIH: 6827 base pairs
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ilarity 69.2%; Pro
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                       TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
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Matches 386; Conserva
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RESULT 7 US-09-954-531-1383

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APPLICANT: Weaver, Zoe TillE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C INVENTION: Gene Sets FILE OF INVENTION: Gene Sets FILE REFERENCE: 689290-77 CURRENT APPLICATION NUMBER: US/09/954,531
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PRICE FILING DATE: 2000-09-18
PRICE FILING DATE: 2000-09-20
PRICE FILING DATE: 2000-09-20
PRICE RELING DATE: 2000-09-20
PRICE PELING DATE: 2000-09-20
PRICE FILING DATE: 2000-09-20
PRICE FILING DATE: 2000-09-20
PRICE FILING DATE: 2000-09-22
PRICE FILING DATE: 2000-09-22
PRICE FILING DATE: 2000-09-22
Sequence 1383, Application US/09954531 Patent No. US20020165180A1 GENERAL INFORMATION:
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SCHIWARE: Patentin version 3.0
SEQ ID NO 1383
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ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
CIIY: New York
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Patent No. US20020072077A1
GENERAL INFORMATION:
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2343 CCAGGIGGCAAAGGGCAIGGCIITICCICGCCICCAAGAATIGIAIICACAGAGACIIGGC 2402
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Pred. No. 3.4e-55;
0; Mismatches 440;
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TILLE OF INVENTION: Sets
FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT PILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR PELING DATE: 2000-09-28
PRIOR PELING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
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Best Local Similarity 55.8%;
Matches 595; Conservative
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US-09-967-768A-277
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GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
APPLICANT: Lemischka, TOTIPOTENT HEMATOPOIETIC STEM CELL
IIILE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1908 AICAGGIGCIIIIGGAAAASIGAIGAACGCAACAGCIIAIGGAAIIASCAAAACAGGAGI 1957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 3501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 249.4; DB 10; Length
Pred. No. 1.9e-63;
0; Mismatches 421; Indels
                                                                                                                                                         Version #1.25
                                                                                                                                                                                                                                                                                                          FILING DATE: «Unknown»
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-UN-1992
APPLICATION: NUMBER: US PCT/US92/05401
FILING DATE: 26-UN-1992
APPLICATION NUMBER: IW 81102961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCI/US92/02750
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 15-APR-1992
APPLICATION NUMBER: US PCI/US92/027;
FILING DATE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
APPLICATION NUMBER: US 07/83,065
FILING DATE: 15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/919.408
FILING DATE: 31-Jul-2001
CLASSIFICATION: <UNKNOWN>
                                                                                     MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC COMPUTED
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/977,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: sig_peptide
LOCAIION: 58..138
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 3501 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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139..3035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Feit, Irving N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
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58..3039
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Best Local Similarity 55.9%;
Matches 572; Conservative (
                                                                                                                                                                                                                                                                    APPLICATION DATA:
                                                                  COMPUTER READABLE FORM:
STATE: New York COUNTRY: U.S.A. ZIP: 10014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO
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                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAIA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inclone Systems Incorporated
STREET: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/906,397
FILLING DATE: 26-JUN-1992
APPLICATION NUMBER: US PCI/US92/05401
FILING DATE: 26-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 15-APR-1992
APPLICATION NUMBER: US PCI/US92/02750
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/208,786
FILING DAIE: <Unknown>
APPLICATION NUMBER: US/09/021,324
                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/872,136
FILING DATE: 01-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                            FILING DAIE: «Unknown»
APPLICATION NUMBER: US/07/977,451
FILING DAIE: 1992-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,055
FILING DATE: 15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DAIE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/728,913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: LEM-3-7P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: TW 81102961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Sig_peptide LOCATION: $8.138 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Feit, Irving N. REGISTRAILON NUMBER: 28,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGIH: 3501 base pairs
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139..3035
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
58..3039
                                                                                                      ZIP: 10014
COMPUTER READABLE FORM:
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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Matches 572; Conservative
                                                                                      COUNTRY: U.S.A.
ZIP: 10014
                                                       New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
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1848 IGAAIAIGAICICAAAIGGGAGTIICCAAGAAAATITAGAGTIGGGAAGGTACIAGG 1907
                                                                                    ICIGALGACTGAGCTAAAAATCTTGACCCACATTGGCCACCATCTGAACGTGGTTAACCT 1031
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                                                                                                                                              912 GIGCCGGACIGIGGCIGIGAAAAIGCIGAAAGAGGGGGCCACGGCCAGCGAGIACAAAGC
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2852 CII 2864

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2031 GCIGGGGCGIGCACACIGICAGGA---CCAAITIACIIGAIITIIGAAIACIGIIGCIA 2087
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Patent No. US20020119494A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   792 TIAIGAIGCCAGCAAGIGGGAGIIIGCCCGGGAGAGACIIAAACIGGGCAAAICACIIGG 851
                                                                                                                                                                                          TITLE OF INVENTION: PROTEIN IYROSINE KINASE AGONISI ANTIBODIES NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  912 GIGCCGGACTGIGGCTGIGAAAAIGCTGAAAGAGGGGGCCACGGCCAGGCGAGIACAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 3120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 422:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 247.8; DB 10
Pred. No. 5.3e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0821P3PCT
                                                                                                                                                                                                                                                                                                                                                                                                            OPERAING SYSIEM: PC_DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,610
FILLNG DATE: 17-Oct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                               ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Brunc Blvd
CITY: South San Francisco
STAIE: Callifornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DAIA:
APPLICATION NUMBER: 09/446,648
FILING DAIE: 1996-MAY-23
APPLICATION NUMBER: 08/222616
FILING DAIE: 04-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
               Sequence 22, Application US/09982610
Patent No. US2002001642001
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
                                                                                                                        Lee, James M.
Matthews, William
Tsai, Siao Ping
Wood, William I.
                                                                     Genentech, Inc.
Bennett, Brian D.
Goeddel, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 3120 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
11.8%;
Best Local Similarity 55.8%;
Matches 571; Conservative
                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
US-09-982-610-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-982-610-22
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1130 TATITITICICAACAAGGAIGCAGCACTACACAIGGAGCCTAAGAAAGAAAAAAGGGGC 1189
                                                                                                                                                                                                                             1190 CAGGCCIGGAACAAGGCAAGAAACCAAGACTAGAIAGCGICACCAGCAGCGAAAGCII-- 1247
                                                                                                                                                                                                                                                                  2208 CAIGCCIGGITCAAGAGAICAGAICAGAICAAAICTCAGGCITCA 2257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1368 GGCCAGAGGCATGGAGTTCCTGTCTTCCAGAAGTGCATTCATCGGGACCTGGCAGCGAG 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2385 IGCCAAAGGAAIGGAAIITCIGGAAIITAAGIGGIGIGIGTATCACAGAGACCIGGCCGCCAG 2444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAACAIICITITAICTGAGAACAACGIGGIGAAGAIITGIGAITITGGCCTIGCCCGGGA 1487
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                                                                                                                                                               2148 GATITICAAGGAACACAATTICAGTTITIACCCCACTTICCAATCACATCCAAATTCCAG 2207
                                                                                                                                                                                                                                                                                                                                              1248 IGCGAGCICCGGCTITCAGGAAGATAAAAGTCTGAGTGATGITGAGGAAGAAGAGGAGGATTC 1307
                                                                                                                                                                                                                                                                                                                                                                                                      2268 IGGGAATICATTICACTCIGAAGATGAAATIGAATATGAAAACCAAAAAAGGCTGGAAGA 2327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2565 GGCCCCCGAAAGCCIGIIIGAAGGCAICTACACCAITAAGAGTGATGTCIGGTCAIAIGG 2624
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IIILE OF INVENTION: Method for identifying substances which positively
IIILE OF INVENTION: influence inflammatory conditions of chronic
IIILE OF INVENTION: inflammatory airway diseases
FILE REFERENCE: 082_00n
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1308 IGACGGIIICIACAAGGAGCCCAICACIAIGGAAGAICIGAITICITACAGIIITCAAGI
1092 IGGAAAICICICCAACIACCICAAGAGGAAAGGIG-----
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CURRENT FILING DAIE: 2001-08-31
PRIOR APPLICATION NUMBER: UK 0021484.1
PRIOR FILING DAIE: 2000-09-01
NUMBER OF SEQ ID NOS: 24
SOFIWARE: PATENTIN VEr. 2.1
SEQ ID NO 9
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                                                                                                                                                                                                                           2020 AAGIGGGAGITCCCCCGGAACAACTGCAGIIIGGIAAGACCTCGGAGCTGGAGCTII 2079
                                                                                                                                                                                                                                                                                                                                                                                                                                  1140 GCIGIGAAGAIGCIGAAGAICCACGGCCCAIGCTGAIGAGAAGGAGGCCCICAIGICCGAG 2199
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                                                                                                                                                                                              805 AAGIGGGAGIIIGCCCGGGAGAGIIAAACIGGGCAAAICACIIGGAAGAGGGGCIIII 864
                                                                                                                                                                                                                                                                                                865 GGAAAAGIGGITCAAGCAICAGCATIIGGCAIIAAGAAAICACCIACGIGCGGACIGIG 924
                                                                                                                                                                                                                                                                                                                                                                                                                984
                                                                                                                                                       9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1105 AACTACCICAAGAGCAAACGIGA---CITAIIITIICICAACAAGGAIGCAGCACTACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTGTGAAAATGCTGAAAGAGGGGGCCACGGCCAGCGAGTACAAAGCTCTGATGACTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2377 CCCGAGGGGGGCGTCGACTATAAGAACATCCACCTCGAGAAGAAATATGTCCGCAGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1222 GAIAGCGICACCAGCAGCGAAAGCITIGCGAGCICCGGCII---ICAGGAAGAIAAAAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2437 AGIGGCIICICCAGCCAGGGIGIGGACACCIAIGIGGAGAIGAGGCCIGICICCACIICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1279 CIGAGIGAIGIIGAGGAAGAGGAGGAIICIGACGGIIICIACAAGGAGCCCAICACIAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2557 CGGGACCTGCTICACTICTCCAGCCAAGACCCAGGGCTICCTCGCCAGG
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                                                                            6: DB 10; Length 3992;
le-58:
                                                                                                                                                 0; Mismatches 444; Indels
                                                                                                  11.1%; Score 233.6;
54.3%; Pred. No. 1e-
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                                                                                          Ouery Match
Best Local Similarity 54.3
Matches 539; Conservative
                     ORGANISM: Homo sapiens
                                             US-09-944-807-9
TYPE: DNA
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AL INFURNATION.
APPLICANT: Lemischka, Ihor R.
IIILE OF INVENTION: TOTIPOIENT HEMATOPOIETIC STEM CELL
RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DAIE: CURKNOWN>
APPLICATION NUMBER: US 07/906,397
FILING DAIE: 26-JUN-1992
APPLICATION NUMBER: US PCT/US92/05401
FILING DAIE: 26-JUN-1992
APPLICATION NUMBER: US 102961
FILING DAIE: 15-APPL1992
APPLICATION NUMBER: US PCT/US92/02750
                                                                                                                                                                                                                                                                                                      ADDRESSEE: Imclone Systems Incorporated STREET: 180 Varick Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-APR-1992
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
2977 ISSSCCIIGGAGCCCACAGAGCCACCTT 3008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/919,408
FILING DAIE: 31-Jul-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKEI NUMBER: LEM-3-7P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DAIE: 28-JUN-1991
APPLICATION NUMBER: US 07/679,666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICE APPLICATION DATA:
APPLICATION NUMBER: 07/977,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 02-APR-1991
                                                                                                                            Sequence 1, Application US/09919408
Patent No. US20020072077A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 3453 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT IYPE: N-terminal
                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                  CIIY: New York
SIAIE: New York
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
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US-09-919-408-1
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1778 AAAGGCCAAGAIIIGCAGAACTIGIGGAAAACIAGGIGAIIIGCIICAAGCAAAIGIAC 1837
                                                                                                                 2834 AGGGGCCAICCTICCCCAACCIGACTICATITITAGGAIGICAGCIGGCAGAGGCAGAAG 2893
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lemischka, Ihor R.
IIILE OF INVENTION: TOTIPOIENT HEMATOPOIETIC STEM CELL
RECEPTORS AND THEIR LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: IMClone Systems Incorporated STREET: 180 Varick Street CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DAIE: 26-JUN-1992
APPLICATION NUMBER: 1W 81102961
FILING DAIE: 15-APR-1992
APPLICATION NUMBER: US PCT/US92/02750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US PCT/US92/05401
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FILING DATE: <Unknown>
APPLICATION NUMBER: US/07/977,451
FILING DATE: 1992-11-19
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/208,786 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DAIE: 24-DEC-1991
APPLICATION NUMBER: US 07/793,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-NOV-1991
APPLICATION NUMBER: US 07/728,913
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APPLICATION NUMBER: US 07/679,666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/872,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 28,501
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DAIA:
                                                                                                                                                                       AACAGGAIGGIAAAGACIACAICC 1861
                                                                                                                                                                                                                      2894 AAGCAIGIAICAGAACAICCAICC 2917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM IYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09872136
Patent No. US20020119545al
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELEPHONE: 212-645-1405
ELEFAX: 212-645-2054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Feit, Irving N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York COUNTRY: U.S.A. ZIP: 10014 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEC ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF
                                                                                                                                                                                                                                                                                           RESULT 14
US-09-872-136-1
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                                                                                                                                                                                      785 GGCICCCITAIGAIGCCAGCAAGIGGGAGIIIGCCCGGGAGAGACIIAAACIGGGCAAAI 844
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                                                                                                  Length 3453;
                                                                                                                                               30;
                                                                                                                                               Indels
                                                                                                DB 10;
                                                                                             Score 221.5; DB 10;
Pred. No. 3.3e-55;
0; Mismatches 489;
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CCATION: 31..3009 SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-919-408-1
                                                                                           Query Match 10.5%;
Best Local Similarity 53.0%;
Matches 585; Conservative
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APPLICANT: INCONO, YASUSHI
TILE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBRCTIC DISEASES
FILE REFERENCE: ERM-104, 0.0
CURRENT APPLICATION NUMBER: US/09/866,510
CURRENT FILING DATE: 2001-05-25
PRIOR PULLOATION NUMBER: 60/250,747
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2001-05-07
NUMBER: 05-07
NUMBER: 05-07
SOFTWARE: PATENTIN OF 2.1
                                                                   GGTCITACGGAGIATIGCIGIGGGAAAICTICCCTIAGGIGGGICTCCAIACCCAGGAG 1557
                                                                                                                                               TACAAATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGGCATGAGGATGAGATCTCTG 1717
                2594 IGRAGIGGAIGGCACCCGAGAGCTTATITGAAGGGATCTACACAATCAAGAGTGACGTCT 2653
                                                                                        2554 GGTCCTACGGCATCCTTCTCTGGGAGATATTTTCACTGGGTGTGAACCCTTACCCTGGCA 2713
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Pred. No. 8.7e-53;
0; Mismatches 486;
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Patent No. US20020111304A1
GENERAL INFORMATION:
APPLICANT: KAZLAUSKAS, ANDRIUS
APPLICANT: IKUNO, YASUSHI
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10.2%;
Best Local Similarity 51.6%;
Matches 621; Conservative (
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                                                                                                                                                                                                                                                                                                                 DB 10; Length 3453;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                               Score 221.5; DB 10;
Pred. No. 3.3e-55;
0; Mismatches 489;
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                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                  mat_peptide
112..3006
                                                                                                                                                         sig_peptide
                                                         FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                               Query Match 10.5%;
Best Local Similarity 53.0%;
Matches 585; Conservative
MOLECULE TYPE: CE
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                 NAME/KEY:
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                                                                           FEATURE:
                                                                                                                                     FEATURE
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Indels

Length 3270;

24	CAAGGAGGCCICIGAIGGIGAIIGIIGAAIACIGCAAAIAIGGAAAICICIC 1103.  ICAGGCCCCAIIIACAICAICAICAACAAGAIIGCIICIAIGGAAAIIIGI 2048	AA	ATCIIIGGAIIGAACCCIGCIGAIGAAAGCACCGGAGCIAIIII	AIITITICICAACAAGGATGCAGCACAAGGAGCCTAAGAAAGAAAAATGGAGCC 1190 11	TTGC 12    	131	CGGITICTACAAGGACCCAICACIATGGAAGAICTGAITICITACAGITITCAAGIGGC 1370 	143	14	ATAAGAACCCGAIIAIGIGAGAAAAGGAGAIACICGACIICCICIGAAAIGGAIGG	TCCCGAAICTAICTIIGACAAAAICIACAGCACCAAGAGGGAGGIGIGGICTIACGGAGI 1519 	ATTOCTOTOGOGAAICTTCTCCTTAGGOGGICTCCATACCCAGGAGTACAAATGGATGA 1670 	GGACTITIGCAGICGCCIGAGGGAAGGCAIGAGGAIGAGAGCICCIGAGTACICITACICC 1730 	179	IGCAGAACTIGIGGAAAACTAGGIGAIIIGCIICAAGCAAAIGIACAACAGGA1SGIAA 1850 	
	44 CACCAAG          92 CACCAAG	4 CAACTACCICAA	1600 09 AGAGCIGGAIAICI	31	91	69	311	371	431	491 529	551 TC    589 TC	611 649	H .6	H . W	H 6	1851 AGA 1853

Search completed: December 8, 2002, 14:45:15 Job time : 200.413 secs

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Am Klopferspitz 18a D-82152 Martinsried, Germany
Ihis is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemannéMarz-heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the German
Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL042601 666 bp mRNA linear EST 29-FEB-2000 DKF2p434L0121_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKF2p434L0121 5', mRNA sequence.
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Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unpublished (1999)
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                                                                 671 ICCIATTAACCCICCTIAICCGAAAAATGAAAAGGICTICTGIGAAAIAAAGACTGACT 730
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697 SCACGCISITIAITGAAAGAGTCACGGAAGAGGATGAAGGCGICTAICACTGCAGACCCA 638
                                           551 CCAACCAGAAGGCCTCTGTGGAAAGTTCAGCATACCTCACTGTTCAAGGAACCTCGGACA 610
                                                                                                                                    611 AGTOTAATOTGGAGOTGATOAGOTGAAOATGCACOTGTGGGGCTGCGACTOTOTTCTGGC 670
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//lab_host="Nector: p17730-Pac (Pharmacia) with a modified
//lab_host="Nector: p17730-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I: Site_2: EcoRI: The MI-P-CPi
library is normalized library derived from the MI-P-CPi
library, ultimately derived from uterus tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
http://pigest.genome.lastate.edu/. The procedure used to
create this library has been previously described (Eccaldo
Lennon and Soares, Genome Research 6: 791-806, 1996)
                                                                                                                                                                                                                                                                             697 bp mRNA linear E對 24-JUN-2002
MI-P-CPI-nzb-m-17-0-UI.Sl MI-P-CPI Sus scrofa cDNA clone
BQ604389
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Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Normalization and subtraction: two approaches to facilitate gene
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                                           Gaps
601 CAGGAAGCTCTGATGATGTCACGATATGTAAATGCTTTCAAGTTCATGAGCCTGGAAAGA 660
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Towa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
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Pred. No. 5.1e-151;
0; Mismatches 76; Indels
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/db_xref="taxon:9823"
/clone="MI-P-CP1"
/clone_lib="MI-P-CP1"
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97044477
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181 c 181 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_LIB=MI-P-CP1
TAG_TISSUE=uterus
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POLYA=Yes.
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89.0%;
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Bonaldo, M.F., Lennor
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No si sequence available.

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/dev_stage="morning" //dev_stage="morning" /
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagāž,M.A., da Silva,M. Jr., Žago,M.A., Bordin,S., Costa,F.F., Coldman,G.H., Carvalho,A.F., Marsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliverra,P.S., Bucher,P., Jorgeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was derived from the FAPESP/LICE Human Cancer Genome Project This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3st2=MR3-GN0186-241155-008-cl0ct3=2000-11-24st4=1)
Seq primer: put 18 forward
High quality sequence stop: 594.
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                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with GRF
                                                                                                                                                                                                                                                                 Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01553-016,
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/clone_lib="GN0186"
                                                                                                                                                                                                                                                                                                                                   Simpson A.J.G.
ory of Cancer Genetics
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1. .650
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 650)
This clone (DKFZp434L0121) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1659 ACAAATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGGCATGAGGGATGAGAGCTCCTGA 1718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1959 TANITCAGGAAGCTCTGATGATGTCAGATATGTAAATGCTTTCAAGTTCATGAGCCTGGA 2018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1839 ACAGGATGGTAAAAACATCCCAATCAATGCCATACTGACAGGAAATAGTGGGGTTTAC 1898
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/tissue_type="testis"
/dov_stage="adult"
/lab_host-"DH106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.7%; Score 561.4; DB 9; 99.8%; Pred. No. 3.4e-148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp434L0121"
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157 g 14
                                                                                                Location/Qualifiers
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146 c la
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Clone_lib="NHEBMA_FIO"

(Lissue_type="whole brain")

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(Abc_
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UI-M-FIO-byw-o-22-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone
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Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-rimail.nih.gov.
lissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: NGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 566)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
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/clone="IMAGE:6400365"
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/db_xeei="Laxon:9606"
/dbone="Lcxon:9606"
/clone="CSOD1061V018"
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/clone=lb="Lrx" NFLO06_PL2"
/clone=lb="Vector: pcNVSDFR 6; Site_l: Not!; ist strand cCNA was primed with a Not!-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Coo RV sites of the pcNVSpCR: 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Peng Liang Life Technologies.
a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20650, USA Fax: (1) 301 610 8371
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li.M.B., Gruber.C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/db_xref="taxon:9606"
/clone="CSODI002Y109"
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/db_xref="taxon.9606"
/clone="CSODIO06FP20"
/tissue_type="placenta"
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was primed with a Not!-oligo(dT) primer. Five prime end
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Liv B., Gruber.C., Jessee, J. and Polayes, D.
Full-length cDNa libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
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AL569839, LTI_NPL006_PL2 Homo sapiens cDNA clone CS0DI002YI09 3 AL569839
enriched, double-stranded cDNA was digested with Not I and cload into the Not I and Eco RV sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies. A division of Invitrogen 5000 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 http://fullength.invitrogen.com*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 540)
1 (M.B., Gruber,C., Jessee.J. and Polayes,D.
Full-length CDNa libraries and normalization.
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 IIACTGCGGACAGTIAATAACAGAACAATGCACTACAGTATTAGCAAGCAAAAAATGGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AICACTAAGGAGCACTCCATCACTTAACCATCATGATGATGTIICCCTGCAAGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GAGGACCIGAAACIGICTIGCACAGIIAACAAGIICTIAIACAGAGAGGGIIACTIGGAIT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 CACAGTGGCCATCAGCAGTTCCACCACTTTAGACTGTCATGCTAATGGTGTCCCCGAGCC 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  627 CACAGIGGCCATCAGCAGITCCACCACITIAGACIGICAILLILLILLILLILLILLILLI
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrel@genoscope.cns.fr. Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                         Length 1005;
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                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                      Score 444.6; DB 9;
Pred. No. 7.4e-115;
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This read is a RESEQUENCE of a proviously sequenced mouse clone. This read has been verified (found to hit its original self in the correct orientation)
                                                                                                                                                                                                                                 Ikis clone is available royalty-free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1522 GATACTCGACTTCCTCTGAAAIGGATGGCTCCCGGAATCIATCTTTGACAAAATCTACAGC 1581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 CACAAAGACCCCAAAGAGAGGCCCCGGTTTGCTGAACTTGTGGAGAAACTTGGTGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib-"Stratagene mouse diaphragm (#937303)*
                                                                                                                Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Lissue_type-"diaphragm"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 20.2%; Score 423.4; DB 9; Best Local Similarity 84.4%; Pred. No. 7.3e-109; Matches 486; Conservative 0; Mismatches 89;
                           Contact: Marra M/Mouse ESI Project
WashU-HHMI Mouse ESI Project
Washington University School of MedicineP
                                                                                                       4414 Förest Park Parkway, Box 8501, St.
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                               Email: mouseest &watson.wusti.edu
                                                                                                                                                                                                                                                                                                                                                                                                  Seg primer: -40kP from Gibco
High quality sequence stop: 410.
Location/Qualifiers
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ORIGIN
JOURNAL
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                  /tissue_type="placenta"
/tissue_type="placenta"
/dote="vector: pcw/SPORT 6; site_1: Notf; ist strand cDNA
was primed with a Notf-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMySiCxI 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: From Liang Lise Technologies.
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filiangelifetech.com URL :
http://fullengalifetech.com URL :
http://fulleng
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostcmi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 855)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Galsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 TTTCATGTTAACTTGGAAAAAATGCCGACGGAAGGAGGAGGACCTGAAACTGTTGCACA 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 ACTTIAGACTGTCATGCTAATGGTGTCCCCGAGCCTCAGATCACTTGGTTTAAAAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 ACANIGCACTACAGIATIAGCAAGCAAAAAATGGCCATCACTAAGGAGCACTCCAICACT
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 442.4; DB 9
Pred, No. 3e-114;
/clone_lib="LTI_NFL006_PL2"
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A1326556.1 GI:4060985
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99.3%;
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VERSION
KEYWORDS
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linear EST 21-AUG-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 606)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-rāmail.nih.gov
Tissue Procurement: Miklos Falkovits, M.D., Fr.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
                                                                                                                                                                                                                                                                                                                                                                                                                                             BI458691 606 bp mRNA linear EST 21-AUG-20
603199829F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5265871 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1056 AGGCCTCTGATGGTGATTGTTGAATACTGCAAATATGGAAATCTCTCCAACTACCTCAA 1115
                                                                                                                           1104 CAACTACCICAAGAGCAAACGIGACIIATITTTTCICAACAAGGAIGCAGCACTACAAC 1163
                                                                                                                                                                                                             1164 GGAGCCTAAGAAAAAAAAGGAGCCAGGCCTGGAACAAGGCAAGAACCAAGACTAGA 1223
                                          1044 CACCAAGCAAGGAGGGCCICIGAIGGIGAITGITGAATACIGCAAAIAIGGAAAICICIC 1103
                                                                                                                                                                                                                                      Toshiyuki and Piero Carninci (RIKEN)
CDNA ilbrary Arrayed by: The T.M.A.G.E. Consortium (LINL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
241 GOTCAAGAICTIGACCCACAICGGCCACCATCIGAAIGICGICAACCIGCIGGGAGCCIG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 406; DB 13; Length 606;
Pred. No. 5.4e-104;
0; Mismatches 10; Indels
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Plate: LLAMIG670 row: i column: 08
High quality sequence start: 2
High quality sequence stop: 604.
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                                                                                                                                                                                                                                                                                                 1224 INGCGICACCAGCAGAGAAGCIIIGCGAGCI 1255
                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NIH_MGC_97"
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                                                                                                                                                                   EST 12-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                   Casas, E.,
                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 512)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Læegreid, W.K. and Keele, J.W.
                                                                                                                                                                                                                                                                                                 Sus scrofa
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pCMV SPORT6: Site_i: NotI; Site_2: SalI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           984 GCTAAAAATCTTGACCCACATTGGCCACCATCTGAACGTGGTTAACCTGCTGGGAGCCTG 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AAG1GGGAGTTTGCCCCGGGAGAGTGTAGCTGGGCAAATCACTGGGAAGAGGGGCTTTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TTCIGTAAAAATGCTGAAAGGGGGCGCCACCGCGGGGGGGGGTACAAAAGCCCTGATGACTGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       924 GGCTGTGAAAATGCTGAAAGAGGGGGCCACGGCCAGCGAGTACAAAGCTCTGATGACTGA 983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 19.8%; Score 415.2; DB 12; Length 512; Best Local Similarity 89.5%; Pred. No. 1.2e-106; Marches 458; Conservative 0; Mismatches 53; Indels 1;
                                                                                                                                           512 bp mRNA linear
303951 WARC IPIG Sus scrofa cDNA 5', mRNA sequence.
BG384715
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
Po Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Eax: 402 762 4390
Email: smithéemail.marc.usda.gov
                      2062 ATGPFTGATGACTACCAGGGCGACAGCAGCACTCTG 2097
                                          540 ATGITTGAGGACTATCAGCTGGACACTAGCACTCTG 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACKWARD: GITTICCCAGTCACGACG
Fiate: 92 row: A column: 16
Seg primer: AITTAGGTGACACTAIAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sus scrofa"
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/lab_host="DH10B"
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Length 561; Indels 60

180

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AL571839 S27 16-FEB-2001 ARNA linear EST 16-FEB-2001 AL571839 LII_NFL006_PL2 Homo sapiens cDNA clone CS0DI030YL03 3
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
(bases 1 to 927)
                                                                                                                                                                                                                                               1522 GATACTCGACTTCCICTGAAATGGATGGCTCCCGGAATCTATCTTTGACAAAATCTACAGC 1581
                                                                                                                                                                                                                                                                                                                     1582 ACCAAGAGCGACJIGTGGTCTIACGGAGTAITGCTGIGGGAAAICIICTCCTTAGGTGGG 1641
                                                                                                                                                                                                                                                                                                                                                                                              1642 ICTCCATACCCAGGAGTACAAATGGATGAGGACTTTTGCAGTCGCCTGAGGGAAGGCATG 1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1702 AGGATGAGAGCTCCTGAGTACTCTACTCCTGAAATCTATCAGAICAIGCTGGACTGCTGG 1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1762 CACAGAGACCCAAAGAAAGGCCAAGATTTGCAGAACTTGTGGAAAAACTAGGTGATTTG 1821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1942 ATTICAGCICCGAAGITTAATICAGGAAGCICTGAIGATGICAGAIAIGIAAAIGCITIC 2001
                                                                                                                                                                                                                                                                                                                                           181 CGGATGAGAACCCGGAGIAIGCCACACCTGAAATCTACCAAATCATGTTGGATTGCTGG 240
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BP 191 91006 EVRY cedex - France
Email: segrefégencscope.ons.fr, Web : www.gencscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                    Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                         Score 385.6; DB 9;
Pred, No. 3.3e-98;
...hag 75;
                                                                                                                 136 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002 AAGTICATGAGCCTGGAAAGAATCAAAACCIT 2033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism~"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESI 04-FEB-1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA066758 561 bp mRNA linear ESI 04-FEB-195
mm09f03.rl Stratagene mouse diaphragm (*937303) Mus musculus cDNA
clone IMAGE:521021 5' similar to 9b:L07297 Mus musculus receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 561)
                                   1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                             176 AGAAAAAATGGAGCCAGGCCTGGAACAAGGCAAGAACCAAGACTAGATAGCGTCACCAG 1235
                                                                                                                                                                                    236 CACCGAAAGCTTTGCGAGCTCCGGCTTTCAGGAAGATAAA-AGTCTGAGTGATGTTGAGG 1294
                                                                                                                                                                                                                                                             AAGAGGAGGATTCTGACGGTTTCTACAAGGAGCCCATCACTAIGG-AAGAICTGATTTCT 1353
                                                                                                                                                                                                                                                                                                                                                                                                            1414 GACCTGGCAGCGAGAAACATTCTTTTATCTGAGAACAACGTGGIGAAGATTTGTGATTTT 1473
                                                                                                                                                                                                                                                                                                                                                                          954
 138 AGGGCCTCTGATGGTGATTG-TGAATACTGCAAATATGGAAATCTCTCCAACTACCTCAA 196
                                                                                                                                   TACAGTITICAAGTGGCCAGAGGCATGGAGTTCCTGTCTTCCAGAAAGTGCATTCATCGG
                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Stratagene mouse diaphragm (*937303)*/tissue_type="diaphragm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :474 GGCCTTGCCCGGGATATTTATAAGAACCCCGATTATGTGAGAAAGGAGATA 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
181: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28ml3 revl ET from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
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Location/Qualifiers
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/rissue_rype="retina"
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/note="Cryan: eye; Vector pCMV-SPORT6; Site_1: NotI;
/note="Cryan: Peep" Vector pCMV-SPORT6; Site_1: NotI;
/note="Cryan: Page and property perioded for primed.
/note="full-length clones and constructed by Life lecinologies.
/note: this is a Nii_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                     17.8%; Score 374.8; DB 13; Length 835; 69.5%; Pred. No. 4.8e-95; Lidels 0; Mismatches 247; Indels 8;
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11913 row: e column: 22
                                                                                              1. .835
/organism="Mus musculus'
                                                                                                                                                                          /clone_lib="NIH_MGC_94"
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                                                                   BI731060 835 bp mRNA linear ESI 20-SEP-2031 603351683F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5355101 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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CDNA Library Arrayed by: The I.M.A.O.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                           78 TTGCACAGTTAACAAGTTCTTATACAGAGGCGTTACTTGGALITTACTGCGGACAGTTAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 TAACAGAACAATGCACTACAGTATTAGCAAGCAAAAAATGGCCATCACTAAGGAGCACTC 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 CATCACTCTTAATCTTACCATCATGAATGTTTCCCTGCAAGATTCAGGCACCTATGCCIG 257
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                                                                                                                                                                                                                                                                                                                             Score 377.4; DB 9;
Pred. No. 9.3e-96;
l; Mismatches, 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
                    /clone="CSODIO30YL03"
/clone_lib="LTI_NFL006_PL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACAACCACAAAATACAACAAGAGCCTGAACT 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 AAACAACCACAAAATACAACAAGAGCCTGGAAT 470
                                                           /tissue_type="placenta"
  /db_xref-"taxon:9606"
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BI731060
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